

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2003, 06:46:52 ; Search time 176 Seconds  
(without alignments)  
1579.785 Million cell updates/sec

Title: US-09-693-205A-7\_COPY\_6543\_6645

Sequence: 1 gaagtgaactgaataacagt.....tcacctgttctgtatccaaca 103

Scoring table: IDENTITY\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
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- 24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NM2002.DAT.\*
- 25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NM2003.DAT.\*

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	103	100.0	12792	22	AAH20176	Human mutated spaaH
2	55.2	53.6	12793	22	AAH20174	Human mutated spaaH
3	55.2	53.6	12793	22	AAH20178	Human mutated spaaH
4	55.2	53.6	12793	22	AAH20179	Human mutated spaaH
5	55.2	53.6	12793	22	AAH20182	Human mutated spaaH
6	53.6	52.0	11493	22	AAH20175	Human mutated spaaH
7	36.2	35.1	1541	22	AAH42107	Mouse spaaH sequence #
8	36.2	35.1	74962	22	AAH15256	Genomic sequence #
C						Human phosphatase

C 9	31.6	30.7	1604	24	ABST9021	E. coli CFT073 gen
C 10	29.4	28.5	31412	25	ABQT5995	Sheep PRP gene nuc
C 11	29.4	28.5	31412	24	ABV99702	Sheep BSE-resistan
C 12	29.2	28.3	148567	23	ABSS55500	Gene encoding huma
C 13	29	28.3	594	25	ABV53300	Human prostate exp
C 14	29	28.2	3080	23	ABL28353	Drosophila melanog
C 15	28.8	28.0	1830121	17	AA742063	Haemophilus influ
C 16	28.6	27.8	3631	23	ABL10204	Drosophila melanog
C 17	28.4	27.6	2341	20	AA383251	Influenza virus PB
C 18	28.4	27.6	41599	21	AA2383193	Consmid including s
C 19	28.2	27.4	804	22	AAH08436	Human CDNA clone (
C 20	28.2	27.4	2362	22	AAH18260	Human CDNA sequenc
C 21	28.2	27.4	3002	21	AA243957	Human DAN CDNA. H
C 22	28.2	27.4	3073	23	ACC46483	Human dltnp nucleot
C 23	28.2	27.4	3078	22	AAK51618	Human polynucleoti
C 24	28.2	27.4	3086	22	AAK52602	Human polynucleoti
C 25	28	27.2	466	21	AAZ64978	Membrane-bound pro
C 26	28	27.2	466	22	AAFA4124	Human EST DNAI6829
C 27	28	27.2	466	25	ABX80189	Novel human secret
C 28	28	27.2	466	25	ABX80693	Human secreted/ttra
C 29	28	27.2	466	25	ABX81076	Novel human secret
C 30	28	27.2	466	25	ABX90166	Human secreted/ttra
C 31	28	27.2	466	25	ABX77777	Human PRO polynuc
C 32	28	27.2	466	25	ABX79373	Human secreted/ttra
C 33	28	27.2	466	25	ABX64012	Human PRO CDNA c
C 34	28	27.2	466	25	ABX16976	Human PRO polynuc
C 35	28	27.2	725	24	ABST6828	Frog embryonic gen
C 36	28	27.2	725	24	ABST6832	Frog embryonic gen
C 37	27.8	27.0	378	22	AAK63709	Human immune/haema
C 38	27.6	26.8	2024	21	AAAC81718	Human secreted pro
C 39	27.6	26.8	2166	22	AAE86585	Alpha-1,3-multi-br
C 40	27.6	26.8	2552	22	AAI88906	Human polynucleoti
C 41	27.6	26.8	2581	15	AAO70104	Bovine enterokinase
C 42	27.6	26.8	3054	24	ABST70481	Human bone remodel
C 43	27.4	26.6	444	23	ABV47128	Human prostate exp
C 44	27.4	26.6	588	25	ABZ41332	N. gonorrhoeae nuc
C 45	27.4	26.6	588	25	ABZ41770	N. gonorrhoeae nuc

## ALIGNMENTS

## RESULT 1

ID AAH20176 standard; DNA; 12792 BP.

AC AAH20176;

DT 09-AUG-2001 (first entry)

Human mutated spastin nucleotide sequence SEQ ID NO:7

KW Human; mouse; spastin; ARSACS; chromosome 13q11; identification;

KW neurodegenerative disease; reduced sensory nerve conduction; diagnosis;

atrophy of upper cerebellar vermis; absence of Purkinje cell;

XXXXXX  
XXXXXX  
XXXXXX

OS Synthetic.

FH	Key	Location/Qualifiers
77	5C04	.

FT / \*tag = a  
EM / \*tag = a

XX  
XX  
E000001000000-00

XX  
XX  
2001-2002

XX 20-OCT-2000: 2000WD-JIC28130  
DE

XX

PR 20-OCT-1999: 99US-0160588.  
XX (UYMC-) UNIV MCGILL.  
PA (HOP-) HOPITAL SAINTE-JUSTINE.  
XX  
XX  
PI Hudson TJ, Engert J, Richter A;  
XX  
DR WPI: 2001-308494/32.  
DR P-PSDB: AAB97821.  
XX  
PT New isolated polynucleotide, encoding spastin gene, and polypeptides,  
PT useful for diagnosing autosomal recessive spastic ataxia of  
PT Charlevoix-Saguenay disease by detecting two point mutations in spastin  
PT gene sequence -  
XX  
XX  
PS Claim 1, Page -: 76pp: English.  
XX  
XX The present invention describes human and mouse spastin, and mutated  
CC human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay  
CC (ARSA) gene sequences (I). The spastin gene has been mapped to  
CC chromosome 13q11. (I) have neuroprotective activities and can be used in  
CC gene therapy and as a spastin polypeptide agonists. (I), their fragments  
CC or their complements can be useful for assaying the presence of a nucleic  
CC acid molecule in a sample. (I) is useful for diagnosing or aiding in the  
CC diagnosis of an early onset neurodegenerative disease in an individual.  
CC The neurodegenerative disease comprises reduced sensory nerve conduction,  
CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres,  
CC atrophy of upper cerebellar vermis, absence of Purkinje cells and  
CC abnormal neuronal lipid storage. (I) can also be used to produce  
CC antisense nucleic acids, is useful as molecular weight or chromosome  
CC markers, to identify genetic disorders, as hybridisation probes or  
CC primers, as an antigen, identify and express recombinant protein for  
CC analysis, characterisation or therapeutic use, or as markers for tissues  
CC in which the corresponding protein is expressed. Diagnostic methods from  
CC the present invention can be used to identify subjects having or at risk  
CC of developing a disease or disorder associated with aberrant expression  
CC or activity of (I). The assays can be utilised to identify a subject  
CC having or at risk of developing a disorder associated with Spastin  
CC protein or spastin gene expression or activity. The present sequence  
CC encodes a mutated human spastin.  
CC N.B. The present sequence is not given in the present specification but  
CC is derived from the human spastin nucleotide sequence (AAH20174) as  
CC stated on page 14.  
XX  
XX  
SQ Sequence 12792 BP; 4163 A; 2256 C; 2487 G; 3886 T; 0 other;  
Query Match 100.0%; Score 103; DB 22; Length 12792;  
Best Local Similarity 100.0%; Pred. No. 5.4e-23;  
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 6543 GAAGTACTGCAATTAACAGTTAATGACAGCATTAATAGCTCCATATGTAATGCT 6602  
QY 61 AATACAGTTAAAAAAGCGTATTTCCTGCTTCTATCCACA 103  
DB 6603 AATACAGTTAAAAAAGCGTATTTCCTGCTTCTATCCACA 6645  
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ID AAH20174 standard: DNA; 12793 BP.  
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XX AAH20174:  
XX  
DT 09-AUG-2001 (first entry)  
XX  
DE Human spastin nucleotide sequence SEQ ID NO:1.  
XX  
XX Human; mouse; spastin: ARSACS; chromosome 13q11; identification;  
KW autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation;  
KW neurodegenerative disease; reduced sensory nerve conduction; diagnosis;  
KW reduced motor nerve velocity; hypermyelination of retinal nerve fibre;

KW atrophy of upper cerebellar vermis; absence of Purkinje cell;  
KW abnormal neuronal lipid storage; genetic disorder; characterisation; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
FH Key Location/Qualifiers  
FT CDS 77..11566  
FT /\*tag= a  
FT /product= "spastin"  
XX  
XX MO200129266-A2.  
XX  
XX 26-APR-2001.  
XX  
XX 20-OCT-2000; 2000MO-US29130.  
XX  
XX  
XX 20-OCT-1999: 99US-0160588.  
XX  
XX  
XX (UYMC-) UNIV MCGILL.  
PA (HOP-) HOPITAL SAINTE-JUSTINE.  
PI Hudson TJ, Engert J, Richter A;  
XX  
XX WPI: 2001-308494/32.  
DR P-PSDB: AAB97819.  
XX  
XX  
PT New isolated polynucleotide, encoding spastin gene, and polypeptides,  
PT useful for diagnosing autosomal recessive spastic ataxia of  
PT Charlevoix-Saguenay disease by detecting two point mutations in spastin  
PT gene sequence -  
XX  
XX  
XX Claim 1, Fig 9; 76pp: English.  
XX  
XX The present invention describes human and mouse spastin, and mutated  
CC human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay  
CC (ARSA) gene sequences (I). The spastin gene has been mapped to  
CC chromosome 13q11. (I) have neuroprotective activities and can be used in  
CC gene therapy and as a spastin polypeptide agonists. (I), their fragments  
CC or their complements can be useful for assaying the presence of a nucleic  
CC acid molecule in a sample. (I) is useful for diagnosing or aiding in the  
CC diagnosis of an early onset neurodegenerative disease in an individual.  
CC The neurodegenerative disease comprises reduced sensory nerve conduction,  
CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres,  
CC atrophy of upper cerebellar vermis, absence of Purkinje cells and  
CC abnormal neuronal lipid storage. (I) can also be used to produce  
CC antisense nucleic acids, is useful as molecular weight or chromosome  
CC markers, to identify genetic disorders, as hybridisation probes or  
CC primers, as an antigen, identify and express recombinant protein for  
CC analysis, characterisation or therapeutic use, or as markers for tissues  
CC in which the corresponding protein is expressed. Diagnostic methods from  
CC the present invention can be used to identify subjects having or at risk  
CC of developing a disease or disorder associated with aberrant expression  
CC or activity of (I). The assays can be utilised to identify a subject  
CC having or at risk of developing a disorder associated with Spastin  
CC protein or spastin gene expression or activity. The present sequence  
CC encodes human spastin as given in the present invention.  
XX  
XX  
SQ Sequence 12793 BP; 4163 A; 2256 C; 2487 G; 3887 T; 0 other;  
Query Match 53.6%; Score 55.2; DB 22; Length 12793;  
Best Local Similarity 75.0%; Pred. No. 8.9e-08;  
Matches 69; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
QY 1 GAAGTACTGCAATTAACAGTTAATGACAGCATTAATAGCTCCATATGTAATGCT 60  
DB 6543 GAAGTACTGCAATTAACAGTTAATGACAGCATTAATAGCTCCATATGTAATGCT 6602  
QY 61 AATACAGTTAAAAAAGCGTATTTCCTGCTT 92  
DB 6603 TAATACAGTTAAAAAAGCGTATTTCCTGCTT 6634  
RESULT 3

AAH20178  
ID AAH20178 standard; DNA: 12793 BP.  
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AC AAH20178:  
XX  
DT 09-AUG-2001 (first entry)  
XX  
DE Human mutated spastin nucleotide sequence SEQ ID NO:11.  
XX  
KW Human; mouse; spastin; ARSACS; chromosome 13q11; identification;  
KW autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation;  
KW neurodegenerative disease; reduced sensory nerve conduction; diagnosis;  
KW reduced motor nerve velocity; hypermyelination of retinal nerve fibre;  
KW atrophy of upper cerebellar vermis; absence of Purkinje cell;  
KW abnormal neuronal lipid storage; genetic disorder; characterisation; ds.  
XX  
OS Homo sapiens.  
OS Synthetic.  
PN WO200129266-A2.  
XX  
PD 26-APR-2001.  
XX  
PF 20-OCT-2000; 2000WO-US29130.  
XX  
PR 20-OCT-1999; 99US-0160588.  
XX  
PA (UYMC-) UNIV MCGILL.  
PA (HOPIT-) HOPITAL SAINTE-JUSTINE.  
XX  
PI Hudson TJ, Engert J, Richter A;  
XX  
DR WPI: 2001-308494/32.  
XX  
PT New isolated polynucleotide, encoding spastin gene, and polypeptides,  
PT useful for diagnosing autosomal recessive spastic ataxia of  
PT Charlevoix-Saguenay disease by detecting two point mutations in spastin  
PT gene sequence -  
XX  
PS Claim 1; Page -: 76pp; English.  
XX  
CC The present invention describes human and mouse spastin, and mutated  
CC human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay  
CC (ARSACS)) gene sequences (I). The spastin gene has been mapped to  
CC chromosome 13q11. (I) have neuroprotective activities and can be used in  
CC gene therapy and as a spastin polypeptide agonists. (I), their fragments  
CC or their complements can be useful for assaying the presence of a nucleic  
CC acid molecule in a sample. (I) is useful for diagnosing or aiding in the  
CC diagnosis of an early onset neurodegenerative disease in an individual.  
CC The neurodegenerative disease comprises reduced sensory nerve conduction,  
CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres,  
CC atrophy of upper cerebellar vermis, absence of Purkinje cells and  
CC abnormal neuronal lipid storage. (I) can also be used to produce  
CC antisense nucleic acids, is useful as molecular weight or chromosome  
CC markers, to identify genetic disorders, as hybridisation probes or  
CC primers, as an antigen, identify and express recombinant protein for  
CC analysis, characterisation or therapeutic use, or as markers for tissues  
CC in which the corresponding protein is expressed. Diagnostic methods from  
CC the present invention can be used to identify subjects having or at risk  
CC of developing a disease or disorder associated with aberrant expression  
CC or activity of (I). The assays can be utilised to identify a subject  
CC having or at risk of developing a disorder associated with Spastin  
CC protein or spastin gene expression or activity. The present sequence  
CC represents a mutated human spastin gene from the present invention.  
CC N.B. The present sequence is not given in the present specification but  
CC is derived from the human spastin nucleotide sequence (AAH20174) as  
CC stated on page 14.  
XX  
SO Sequence 12793 BP; 4163 A; 2255 C; 2487 G; 3888 T; 0 other;

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Best Local Similarity 75.08; Pred. No. 8.9e-08;  
Matches 69; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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DB 6543 GAAGTGACGTGAATACAGTTTAAATGACAGATTATAGCTCGATATGTAATTGCT 6602  
OY 61 AATACAGTTAAAAAAGCGTATTTCCCTGGTT 92  
DB 6603 TAATACAGTTAAAAAAGCGTATTTCCCTGGT 6634  
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XX  
AC AAH20179:  
XX  
DT 09-AUG-2001 (first entry)  
XX  
DE Human mutated spastin nucleotide sequence SEQ ID NO:12.  
XX  
KW Human; mouse; spastin; ARSACS; chromosome 13q11; identification;  
KW autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation;  
KW neurodegenerative disease; reduced sensory nerve conduction; diagnosis;  
KW reduced motor nerve velocity; hypermyelination of retinal nerve fibre;  
KW atrophy of upper cerebellar vermis; absence of Purkinje cell;  
KW abnormal neuronal lipid storage; genetic disorder; characterisation; ds.  
XX  
OS Homo sapiens.  
OS Synthetic.  
PN WO200129266-A2.  
XX  
PD 26-APR-2001.  
XX  
PF 20-OCT-2000; 2000WO-US29130.  
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PR 20-OCT-1999; 99US-0160588.  
XX  
PA (UYMC-) UNIV MCGILL.  
PA (HOPIT-) HOPITAL SAINTE-JUSTINE.  
XX  
PI Hudson TJ, Engert J, Richter A;  
XX  
DR WPI: 2001-308494/32.  
XX  
PT New isolated polynucleotide, encoding spastin gene, and polypeptides,  
PT useful for diagnosing autosomal recessive spastic ataxia of  
PT Charlevoix-Saguenay disease by detecting two point mutations in spastin  
PT gene sequence -  
XX  
PS Claim 1; Page -: 76pp; English.  
XX  
CC The present invention describes human and mouse spastin, and mutated  
CC human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay  
CC (ARSACS)) gene sequences (I). The spastin gene has been mapped to  
CC chromosome 13q11. (I) have neuroprotective activities and can be used in  
CC gene therapy and as a spastin polypeptide agonists. (I), their fragments  
CC or their complements can be useful for assaying the presence of a nucleic  
CC acid molecule in a sample. (I) is useful for diagnosing or aiding in the  
CC diagnosis of an early onset neurodegenerative disease in an individual.  
CC The neurodegenerative disease comprises reduced sensory nerve conduction,  
CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres,  
CC atrophy of upper cerebellar vermis, absence of Purkinje cells and  
CC abnormal neuronal lipid storage. (I) can also be used to produce  
CC antisense nucleic acids, is useful as molecular weight or chromosome  
CC markers, to identify genetic disorders, as hybridisation probes or  
CC primers, as an antigen, identify and express recombinant protein for  
CC analysis, characterisation or therapeutic use, or as markers for tissues  
CC in which the corresponding protein is expressed. Diagnostic methods from  
CC the present invention can be used to identify subjects having or at risk  
CC of developing a disease or disorder associated with aberrant expression  
CC or activity of (I). The assays can be utilised to identify a subject  
CC having or at risk of developing a disorder associated with Spastin

CC protein or spastin gene expression or activity. The present sequence  
CC encodes a mutated human spastin.  
CC N.B. The present sequence is not given in the present specification but  
CC is derived from the human spastin nucleotide sequence (AAH20174) as  
CC stated on page 14.  
XX  
SQ Sequence 12793 BP; 4163 A; 2257 C; 2487 G; 3886 T; 0 other:  
Query Match 53.6%; Score 55.2; DB 22; Length 12793;  
Best Local Similarity 75.0%; Pred. No. 8.9e-08;  
Matches 69; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
OY 1 GAAGTCACTGGAATAACACTTTAATGACAGCATTAATACCTCTGCATATGCAATTGCT 60  
DB 6543 GAAGTCACTGGAATAACACTTTAATGACAGCATTAATACCTCTGCATATGTTGAATTGC 6602  
OY 61 AATACAGTTAAAAAACGCTATTTCCTCGTT 92  
DB 6603 CAATACAGTTAAAAAACGCTATTTCCTCGT 6634  
RESULT 5  
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XX  
AC AAH20182;  
XX  
DT 09-AUG-2001 (first entry)  
XX  
DE Human mutated spastin nucleotide sequence SEQ ID NO:15.  
XX  
KW Human; mouse; spastin; ARSACS; chromosome 13q11; identification;  
KW autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation;  
KW neurodegenerative disease; reduced sensory nerve conduction; diagnosis;  
KW reduced motor nerve velocity; hypermyelination of retinal nerve fibre;  
KW atrophy of upper cerebellar vermis; absence of Purkinje cell;  
KW abnormal neuronal lipid storage; genetic disorder; characterisation; ds.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT CDS 77..11566  
FT /\*tag= a  
FT /product= "mutated spastin"  
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XX WO200129266-A2.  
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XX 26-APR-2001.  
XX  
XX 20-OCT-2000; 2000WO-US29130.  
XX  
XX 20-OCT-1999; 99US-0160588.  
XX  
XX (UVMC-) UNIV MCGILL.  
XX (HOPI-) HOPITAL SAINTE-JUSTINE.  
XX  
XX Hudson TJ, Engert J, Richter A;  
XX  
XX WPI; 2001-308494/32.  
XX  
XX P-PSDB; AAB97823.  
XX  
XX New isolated polynucleotide, encoding spastin gene, and polypeptides,  
XX useful for diagnosing autosomal recessive spastic ataxia of  
XX Charlevoix-Saguenay disease by detecting two point mutations in spastin  
XX gene sequence -  
XX  
XX Claim 1; Page -: 76pp; English.  
XX  
XX The present invention describes human and mouse spastin, and mutated  
XX human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay  
XX (ARSACS)) gene sequences (1). The spastin gene has been mapped to  
XX chromosome 13q11. (1) have neuroprotective activities and can be used in

CC gene therapy and as a spastin polypeptide agonists. (1), their fragments  
CC or their complements can be useful for assaying the presence of a nucleic  
CC acid molecule in a sample. (1) is useful for diagnosing or aiding in the  
CC diagnosis of an early onset neurodegenerative disease in an individual.  
CC The neurodegenerative disease comprises reduced sensory nerve conduction,  
CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres,  
CC atrophy of upper cerebellar vermis, absence of Purkinje cells and  
CC abnormal neuronal lipid storage. (1) can also be used to produce  
CC antisense nucleic acids, is useful as molecular weight or chromosome  
CC markers, to identify genetic disorders, as hybridisation probes or  
CC primers, as an antigen, identify and express recombinant protein for  
CC analysis, characterisation or therapeutic use, or as markers for tissues  
CC in which the corresponding protein is expressed. Diagnostic methods from  
CC the present invention can be used to identify subjects having or at risk  
CC of developing a disease or disorder associated with aberrant expression  
CC or activity of (1). The assays can be utilised to identify a subject  
CC having or at risk of developing a disorder associated with Spastin  
CC protein or spastin gene expression or activity. The present sequence  
CC encodes a mutated human spastin.  
CC N.B. The present sequence is not given in the present specification but  
CC is derived from the human spastin nucleotide sequence (AAH20174) as  
CC stated on page 14.  
XX  
SQ Sequence 12793 BP; 4163 A; 2257 C; 2487 G; 3886 T; 0 other:  
Query Match 53.6%; Score 55.2; DB 22; Length 12793;  
Best Local Similarity 75.0%; Pred. No. 8.9e-08;  
Matches 69; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
OY 1 GAAGTCACTGGAATAACACTTTAATGACAGCATTAATACCTCTGCATATGCAATTGCT 60  
DB 6543 GAAGTCACTGGAATAACACTTTAATGACAGCATTAATACCTCTGCATATGTTGAATTGC 6602  
OY 61 AATACAGTTAAAAAACGCTATTTCCTCGTT 92  
DB 6603 TAATACAGTTAAAAAACGCTATTTCCTCGT 6634  
RESULT 6  
ID AAH20175 standard; DNA; 11493 BP.  
XX  
XX  
AC AAH20175;  
XX  
DT 09-AUG-2001 (first entry)  
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DE Mouse spastin nucleotide sequence SEQ ID NO:3.  
XX  
XX Human; mouse; spastin; ARSACS; chromosome 13q11; identification;  
KW autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation;  
KW neurodegenerative disease; reduced sensory nerve conduction; diagnosis;  
KW reduced motor nerve velocity; hypermyelination of retinal nerve fibre;  
KW atrophy of upper cerebellar vermis; absence of Purkinje cell;  
KW abnormal neuronal lipid storage; genetic disorder; characterisation; ds.  
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XX Mus musculus.  
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XX  
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XX CDS 1..11493  
XX /\*tag= a  
XX /product= "spastin"  
XX  
XX WO200129266-A2.  
XX  
XX 26-APR-2001.  
XX  
XX 20-OCT-2000; 2000WO-US29130.  
XX  
XX 20-OCT-1999; 99US-0160588.  
XX  
XX (UVMC-) UNIV MCGILL.  
XX (HOPI-) HOPITAL SAINTE-JUSTINE.  
XX  
XX



PI Hudson TJ, Engert J, Richter A;  
XX  
DR WPI: 2001-308494/32.  
DR P-PSDB; AAB97820.  
PT New isolated polynucleotide, encoding spastin gene, and polypeptides,  
PT useful for diagnosing autosomal recessive spastic ataxia of  
PT Charlevoix-Saguenay disease by detecting two point mutations in spastin  
PT gene sequence -  
XX  
PS Claim 1; Fig 8; 76pp; English.  
XX  
CC The present invention describes human and mouse spastin, and mutated  
CC human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay  
CC (ARSA) gene sequences (I). The spastin gene has been mapped to  
CC chromosome 13q11. (I) have neuroprotective activities and can be used in  
CC gene therapy and as a spastin polypeptide agonists. (I), their fragments  
CC or their complements can be useful for assaying the presence of a nucleic  
CC acid molecule in a sample. (I) is useful for diagnosing or aiding in the  
CC diagnosis of an early onset neurodegenerative disease in an individual.  
CC The neurodegenerative disease comprises reduced sensory nerve conduction,  
CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres,  
CC atrophy of upper cerebellar vermis, absence of Purkinje cells and  
CC abnormal neuronal lipid storage. (I) can also be used to produce  
CC antisense nucleic acids, is useful as molecular weight or chromosome  
CC markers, to identify genetic disorders, as hybridisation probes or  
CC primers, as an antigen, identify and express recombinant protein for  
CC analysis, characterisation or therapeutic use, or as markers for tissues  
CC in which the corresponding protein is expressed. Diagnostic methods from  
CC the present invention can be used to identify subjects having or at risk  
CC of developing a disease or disorder associated with aberrant expression  
CC or activity of (I). The assays can be utilised to identify a subject  
CC having or at risk of developing a disorder associated with Spastin  
CC protein or spastin gene expression or activity. The present sequence  
CC encodes mouse spastin as given in the present invention.  
XX  
SQ Sequence 11493 BP; 3599 A; 2281 C; 2387 G; 3226 T; 0 other;  
XX  
Query Match 52.0%; Score 53.6; DB 22; Length 11493;  
Best Local Similarity 73.9%; Pred. No. 2.8e-07;  
Matches 68; Conservative 0; Mismatches 24; Indels 0; Gaps 0;  
OY 1 GAAGTGCATGGAATTAACAGTTTAAATGACACATTAAATAGCTCGATGTAATGCT 60  
DB 6467 GAAGTGCATGGAATTAATAGTTTAAATGACACATTAAATAGACCTGATGTAATG 6526  
OY 61 AATACAGTTAAATAAACGGTATTTCCCTGGT 92  
DB 6527 TAATCCAGTTAAATAAACGGTATTTCCCTGGT 6558  
RESULT 7  
AAS42107 standard; DNA; 1541 BP.  
XX  
AC AAS42107;  
XX  
DT 17-DEC-2001 (first entry)  
XX  
DE Genomic sequence #423 encoding novel human enzyme polypeptide.  
XX  
KW Human: oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;  
KW ligase; hyperproliferative disorder; immunodeficiency disorder;  
KW autoimmune disorder; neurological disorder; metabolic disorder;  
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;  
KW blood-related disorder; infectious disorder; gene therapy; cytostatic;  
KW anti arthritic; nephrotropic; anticoagulant; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200155301-A2.  
XX  
PD 02-AUG-2001.

XX  
PF 17-JAN-2001; 2001WO-US01239.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226868.  
PR 23-AUG-2000; 2000US-0227182.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0232403.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.

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PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI, 2001-465566/50.
XX

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PT Novel polypeptides and polynucleotides useful for diagnosing,
PT preventing, treating neural, immune system, muscular, reproductive,
PT pulmonary, cardiovascular, renal, proliferative disorders and cancerous
PT diseases
XX
PS Disclosure; SEQ ID No 2233; 1180bp; English.
XX
XX The present invention relates to the isolation of novel human enzyme
CC polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the
CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC disorders including hyperproliferative disorders (e.g. cancer),
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders
CC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),
CC metabolic disorders (e.g. phenylketonuria), inflammatory disorders
CC (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),
CC blood-related disorders (e.g. haemophilia), reproductive disorders
CC (e.g. infertility) and infectious disorders (e.g. influenza). The
CC polynucleotides of the invention can also be used in gene therapy.
CC AAS41685-AAS42192 represent DNA sequences encoding for the novel human
CC enzyme polypeptides of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1541 BP; 552 A; 267 C; 252 G; 470 T; 0 other:

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OY Query Match 35.1%; Score 36.2; DB 22; Length 1541;
DB Best Local Similarity 62.9%; Pred. No. 0.066;
Matches 56; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
OY 12 AATAACAGTTTATGACGACATTAAATGCTGATATGCTAATGCTAATACAGTTAA 71
DB 395 AAAAAAAAAAATTCACGATTCACAAACCCCTAGAGACTTCTTTCTAATCAATTA 454
OY 72 AAAAAAGTATTTCCCTGGTCTGATCCCA 100
DB 455 AAAAAAGCTTCTTCAGTACTTCTCATCTCA 483

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RESULT 8
AADI5256/c
ID AADI5256 standard; DNA; 74962 BP.
XX
XX AADI5256;
AC
XX
XX 15-NOV-2001 (first entry)
DT
XX
XX Human phosphatase gene.
DE
XX
XX Human; tyrosine phosphatase subfamily; cellular process modulation;
KW phosphatase; chromosome 14; single nucleotide polymorphism; SNP;
XX variant; ds.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX CDS 19364..59833
XX
XX /*tag= a
XX /product= "Human phosphatase protein"
XX /replace (3114, A)
XX /*tag= b
XX /standard.name= "Single nucleotide polymorphism (SNP)"
XX /note= "Polymorphic site 1"
XX /replace (4004, A)
XX /*tag= c
XX /standard.name= "Single nucleotide polymorphism (SNP)"
XX /note= "Polymorphic site 2"
XX /replace (4514, G)
XX /*tag= d
XX /standard.name= "Single nucleotide polymorphism (SNP)"
XX

```



CC The present invention provides phosphatase peptides, proteins and  
CC their polynucleotides. The phosphatase proteins are related to the  
CC protein tyrosine phosphatase subfamily. The peptides of the invention  
CC are useful for identifying a modulator of phosphatase peptide expression.  
CC Modulators of phosphatase peptide are useful for treating diseases or  
CC conditions mediated by a human phosphatase protein. The phosphatase gene  
CC of the present invention can be expressed in yeast to identify possible  
CC interactors and substrates. Artificially synthesised enzymes or derived  
CC peptides can be used to activate or inhibit cellular processes modulated  
CC by this phosphatase. The present sequence is a human gene encoding  
CC phosphatase protein. This gene is located on human chromosome 14.  
XX  
SQ Sequence 74962 BP; 21639 A; 14055 C; 14307 G; 24824 T; 137 other:  
Query Match 35.1%; Score 36.2; DB 22; Length 74962;  
Best Local Similarity 62.9%; Pred. No. 0.14;  
Matches 56; Conservative 0; Mismatches 33; Indels 0; Gaps 0;  
QY 12 AATACAGTTTATACAGCATTTATACCTCTGATATGTAATGCTAATACAGTTAA 71  
DB 63338 AAAAAAAAAAAATTCAGCATTCAGAGCCCTAGAGACTTACTTCTAATCAATTTAA 63279  
QY 72 AAAAAAGCTATTTCCCTGCTCTGATCCA 100  
DB 63278 AAAAAAGCTTTCAGTACTTCTCATCTA 63250  
RESULT 9  
ABST9021/C  
ID ABST9021 standard; DNA; 1604 BP.  
XX  
AC ABST9021;  
XX  
DT 17-DEC-2002 (first entry)  
XX  
DE E. coli CFT073 genomic sequence #188.  
XX  
KM Pathogenic; Escherichia coli CFT073 infection; livestock; pyelonephritis;  
KM urinary tract infection; open reading frame; ORF; uropathogenic;  
KM antibacterial; atrophic; nephrotropic; gene; ds.  
XX  
OS Escherichia coli.  
XX  
PN WO200259320-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 19-OCT-2001; 2001WO-US46833.  
XX  
PR 19-OCT-2000; 2000US-242412P.  
XX  
PA (WISC ) WISCONSIN ALUMNI RES FOUND.  
XX  
PI Blattner FR, Welch RA, Burland VD;  
XX  
DR WPI: 2002-691532/74.  
XX  
PT New DNA sequences of the pathogenic Escherichia coli CFT073 strain,  
PT useful for preventing or treating E. coli CFT073 infection in humans or  
PT livestock  
XX  
PS Claim 1; Page 566; 765pp; English.  
XX  
CC The present invention relates to polynucleotide sequences from the  
CC genome of the pathogenic Escherichia coli strain CFT073. Almost all  
CC the sequences present in E. coli CFT073 are absent in the previously  
CC sequenced laboratory strain K-12. The polynucleotide sequences of  
CC the invention are useful for preventing, diagnosing or treating  
CC E. coli CFT073 infection in humans or livestock. The polynucleotide  
CC sequences are useful for preventing urinary tract infections and  
CC pyelonephritis. Likewise, the polypeptides encoded by the different  
CC open reading frames (ORF1-5) are useful for generating a vaccine  
CC against uropathogenic E. coli strains. ABST9834-ABST9085 represent

CC genomic sequences from E. coli strain CFT073.  
XX  
SQ Sequence 1604 BP; 534 A; 247 C; 276 G; 547 T; 0 other:  
QY  
Query Match 30.7%; Score 31.6; DB 24; Length 1604;  
Best Local Similarity 56.9%; Pred. No. 1.9;  
Matches 58; Conservative 0; Mismatches 44; Indels 0; Gaps 0;  
QY 2 AAGTACGTGAATTAACAGTTTATGACAGCATTAATACCTCGCATATGTAATGCTA 61  
DB 1130 AAGTCAATGATATGATATTTTTCGCAAAATGAAAGATCTGGCAAAATGTTTCTT 1071  
QY 62 ATACAGTAAAAAAGGTATTTCCCTGCTCTGATCCAACA 103  
DB 1070 TTTTGACAAATATCAAAACATCATCAGAGATCTGATGATCA 1029  
RESULT 10  
ABQ75995/C  
ID ABQ75995 standard; DNA; 31412 BP.  
XX  
AC ABQ75995;  
XX  
DT 05-NOV-2002 (first entry)  
XX  
DE Sheep PRP gene nucleic acid sequence.  
XX  
KM Sheep; PRP; prion; transmissible spongiform encephalopathy; TSE; scrapie;  
KM breeding; selection; gene; ds.  
XX  
OS Ovis aries.  
XX  
PN GB2371048-A.  
XX  
PD 17-JUL-2002.  
XX  
PF 10-JAN-2001; 2001GB-0000702.  
XX  
PR 10-JAN-2001; 2001GB-0000702.  
XX  
PA (UYYO-) UNIV YORK.  
XX  
PI Ross J, Bowles D;  
XX  
DR WPI: 2002-577556/62.  
XX  
PD Assay for comparing nucleic acid sequence with a reference, useful for  
PD determining prion gene alleles, comprises determining the profile of  
PD heteroduplexes  
XX  
PS Claim 2 (1)(a); Fig 1; 36pp; English.  
XX  
CC The invention relates to an assay for determining allelic variations in  
CC prion protein genes, involving comparing a nucleic acid sequence with a  
CC reference. The method is used for determining the PRP allele in an animal  
CC (or human) in order to assess susceptibility to transmissible spongiform  
CC encephalopathies (TSE), most especially scrapie in sheep. This assists in  
CC the selection, for breeding, of animals having the alleles known to be  
CC associated with lowest risk. The method is reproducible and rapid,  
CC provides high resolution between allelic variants and is suitable for  
CC processing large numbers of samples. The current sequence represents a  
CC sheep PRP gene, that is used in the context of the invention as a  
CC comparison nucleic acid.  
XX  
SQ Sequence 31412 BP; 8889 A; 6517 C; 6464 G; 9542 T; 0 other:  
Query Match 28.5%; Score 29.4; DB 24; Length 31412;  
Best Local Similarity 63.4%; Pred. No. 17;  
Matches 45; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
QY 13 ATACAGTTTATGACAGCATTAATACCTCGCATATGTAATGCTAATACAGTTAA 72  
DB 21603 ATATCTGTTAATGAGAAATTAACATCTCTCAACATATTAATGCAACAAATTTTA 21544





XX 17-SEP-2002 (first entry)  
 DT Human prostate expression marker cDNA 53291.  
 XX  
 DE Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.  
 KM  
 XX Homo sapiens.  
 OS  
 PN WO200160860-A2.  
 PD  
 XX 23-AUG-2001.  
 XX  
 PF 20-FEB-2001; 2001WO-US05171.  
 XX  
 PR 17-FEB-2000; 2000US-183319P.  
 PR 16-MAR-2000; 2000US-189862P.  
 PR 25-MAY-2000; 2000US-207454P.  
 PR 09-JUN-2000; 2000US-211314P.  
 PR 18-JUL-2000; 2000US-219007P.  
 PR 13-DEC-2000; 2000US-235281P.  
 XX  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX  
 PI Schlegel R, Endege WO, Monahan JE;  
 DR WPI; 2001-662795/76.  
 XX  
 PT Novel isolated nucleic acid molecule associated with cancerous state of  
 PT prostate cells and correlating with presence of prostate cancer, useful  
 PT for detecting presence of prostate cancer, stage of prostate cancer -  
 XX  
 PS Claim 1; Page 10326; 11750pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
 CC specification or its complement. (I) is useful for:  
 CC (a) assessing whether a patient is afflicted with prostate cancer;  
 CC (b) monitoring the progression of prostate cancer in a patient;  
 CC (c) assessing the efficacy of a test compound to inhibit prostate  
 CC cancer in a patient;  
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
 CC in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound;  
 CC (g) determining whether prostate cancer has metastasized in a patient;  
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
 CC patient;  
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.  
 XX  
 SQ Sequence 594 BP; 155 A; 150 C; 102 G; 186 T; 1 other:  
 Query Match 28.2%; Score 29; DB 23; Length 594;  
 Best Local Similarity 58.8%; Pred. No. 11;  
 Matches 50; Conservative 0; Mismatches 35; Indels 0; Gaps 0;  
 OY 1 GAAGTACTGGAATACAGTTTAATGACAGCATTAAAGCTCTGCAATGAGTAATGCT 60  
 DB 446 GAGGTGCGCTGGAATCTTAAGTTTACAGAAAGCATTAAAGTATGATCTTTCTCTCTT 505  
 OY 61 AATACAGTAAAAAAGCGTATTTTC 85  
 DB 506 TATCCATTGTAAGACAGGATCTTC 530

RESULT 14  
 ABL28356  
 ID ABL28356 standard; DNA; 3080 BP.  
 XX  
 AC ABL28356;  
 XX  
 DT 26-MAR-2002 (first entry)

XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 36541.  
 DE  
 XX Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical; gene; ds.  
 KM  
 XX Drosophila melanogaster.  
 OS  
 PN WO200171042-A2.  
 PD  
 XX 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-US09231.  
 XX  
 PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 DR WPI; 2001-656860/75.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX  
 PS Claim 1; SEQ ID NO 36541; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA  
 CC sequences (AB101840-AB16175) and the encoded proteins  
 CC (AB857737-AB872072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 3080 BP; 834 A; 745 C; 726 G; 775 T; 0 other:  
 Query Match 28.2%; Score 29; DB 23; Length 3080;  
 Best Local Similarity 63.8%; Pred. No. 15;  
 Matches 44; Conservative 0; Mismatches 25; Indels 0; Gaps 0;  
 OY 24 ATGACAGCATTAAAGCTCTGATATGTAATTGCTAATACAGTTAAAAAGCGTATT 83  
 DB 438 AAGCTAAGTTCATTAAGCTATTCATGACAGCGCTAATCATTTAATGCAATT 497  
 OY 84 TCCTCGGTT 92  
 DB 498 TCCCTTTT 506

RESULT 15  
 AAT42063/c  
 ID AAT42063 standard; DNA; 1830121 BP.  
 XX  
 AC AAT42063;  
 XX  
 DT 14-SEP-1999 (first entry)  
 DE Haemophilus influenzae complete genome sequence.  
 DE  
 KW Genome; bacterium; Haemophilus influenzae; computer readable medium;  
 KW expression modulating fragment; regulation; gene expression; vector;  
 KW organism; open reading frame; ORF; ds.  
 XX  
 OS Haemophilus influenzae.  
 XX  
 PN WO9633276-A1.

XX 24-OCT-1996.  
 PD 22-APR-1996; 96WO-US05320.  
 XX  
 PF 07-JUN-1995; 95US-0487429.  
 PR 21-APR-1995; 95US-0426787.  
 PR 07-JUN-1995; 95US-0476102.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Adams MD, Fleischmann RD, Smith HO, Venter JC, White O;  
 XX WPI; 1996-485782/48.  
 DR  
 XX Haemophilus influenzae Rd genome recorded on computer readable  
 PT medium - useful for identifying commercially important nucleic acid  
 PT fragments by homology searching  
 XX  
 PS Claim 1; Page 77.2-77.1091; 1291pp; English.  
 XX  
 CC This sequence represents the complete genome sequence of the bacterium  
 CC Haemophilus influenzae strain Rd. The invention relates to a computer  
 CC readable medium (CRM) having recorded upon it the complete H. influenzae  
 CC nucleotide sequence (I), a representative fragment of (I) or a nucleotide  
 CC sequence at least 9% identical to (I). By providing the full-length  
 CC genomic sequence in a computer readable form, it is possible to identify  
 CC commercially important nucleic acid fragments and expression modulating  
 CC fragments (EMFs) of the Haemophilus genome. The EMFs can be used to  
 CC regulate the expression of a nucleic acid molecule. Vectors and altered  
 CC organisms comprising the predicted ORFs can be used to produce any of the  
 CC polypeptide fragments of the H. influenzae Rd genome.  
 XX  
 SQ Sequence 1830121 BP; 567399 A; 350615 C; 347389 G; 564036 T; 682 other;  
 Query Match 28.0%; Score 28.8; DB 17; Length 1830121;  
 Best Local Similarity 58.0%; Pred. No. 59;  
 Matches 51; Conservative 0; Mismatches 37; Indels 0; Gaps 0;  
 QY 13 ATAAAGCTTTAATGACAGCATTAATAGCTCCTGCATATGTAATGCTAATACAGTTAA 72  
 DB 1541231 ATTAAGAGAGCTGTTTTCATTAATAGTTAGTGTATTTTCATTTTCATTTAAAT 1541172  
 QY 73 AAAACGGATTTTCCCTGTTCTGATCCA 100  
 DB 1541171 AAAAATATATATCTCTATTCATCA 1541144  
 RESULT 16  
 ABL10204/C  
 ID ABL10204 standard; CDNA; 3631 BP.  
 XX  
 AC ABL10204;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 25094.  
 XX  
 KW Drosophila: developmental biology; cell signalling; insecticide;  
 KW pharmaceutical; gene; ss.  
 XX  
 OS Drosophila melanogaster.  
 OS  
 PN WO200171042-A2.  
 PN  
 XX 27-SEP-2001.  
 PD  
 XX 23-MAR-2001; 2001WO-US09231.  
 PF  
 XX 23-MAR-2000; 2000US-191637P.  
 PR  
 XX 11-JUL-2000; 2000US-0614150.  
 PT  
 XX

PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX  
 DR WPI; 2001-656860/75.  
 DR P-PSDB; ABB6101.  
 XX  
 XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions  
 XX  
 XX Claim 1; SEQ ID NO 25094; 21pp + Sequence Listing; English.  
 PS  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB101840-AB116175), expressed DNA  
 CC sequences (AB101840-AB116175) and the encoded proteins  
 CC (AB57737-AB572072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pcf\_sequences.  
 XX  
 SQ Sequence 3631 BP; 1115 A; 691 C; 711 G; 1114 T; 0 other;  
 Query Match 27.8%; Score 28.6; DB 23; Length 3631;  
 Best Local Similarity 59.0%; Pred. No. 21;  
 Matches 49; Conservative 0; Mismatches 34; Indels 0; Gaps 0;  
 QY 2 AAGTACGTGGAATTAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTAATGCTA 61  
 DB 2172 AATGTTGCTATGTAACCTTTACAGTTAATATTAATGCTGCTAATATTAATATA 2113  
 QY 62 ATACAGTTAAAAAAGCGTATTT 84  
 DB 2112 TTATAGTTAAATGAACGGTAAT 2090  
 RESULT 17  
 AAX82193  
 ID AAX82193 standard; DNA; 2341 BP.  
 XX  
 AC AAX82193;  
 XX  
 DT 18-AUG-1999 (first entry)  
 XX  
 DE Influenza virus PB1 protein gene sequence.  
 XX  
 KW Cold-adapted Influenza virus; passage culture; PB2 protein; PB1 protein;  
 KW PA protein; NP protein; M protein; NS protein; temperature sensitivity;  
 KW vaccine; flu; influenza; ss.  
 XX  
 OS Influenza virus.  
 OS  
 PN WO9928445-A1.  
 PN  
 XX 10-JUN-1999.  
 PD  
 XX 30-NOV-1996; 96WO-KR00384.  
 PF  
 XX 29-NOV-1997; 97KR-0064854.  
 PR  
 XX (CHEI-) CHEIL JEDANG CORP.  
 XX  
 PI Cheoun KH, Kim HG, Kim J, Kim SJ, Lee KH, Seong BL;  
 PI Youn JW;  
 XX  
 DR WPI; 1999-385377/32.  
 DR  
 XX Cold-adapted Influenza viruses useful for the production of  
 PT protective vaccines against flu



XX PS Claim 4; Page 52-53; 62pp; English.

CC The invention relates to cold-adapted influenza viruses prepared by  
CC passage culture of A/X-31, B/Yamagata/16/88 or B/Lee/40 viruses at low  
CC temperatures. A cDNA gene of cold-adapted influenza virus H7CA-A101 can  
CC be selected from a group consisting of PB2 protein gene, PB1 protein  
CC gene, PA protein gene, NP protein gene, M protein gene and NS protein  
CC gene (AA82192-x82197). The method is useful for the production of cold-  
CC adapted influenza virus that exhibit temperature sensitivity and can be  
CC actively grown in fertilized eggs. The virus is useful for vaccines for  
CC protection against flu. Live vaccines containing cold-adapted viruses  
CC have several advantages over killed vaccines. It can prevent reduction  
CC of immunogenicity, which may occur in the killed vaccine where antigenic  
CC proteins would be denatured at its inactivation. It can also avoid  
CC hypersensitivity due to the prolonged administration of heterologous  
CC proteins. It promotes the immunity by inducing IgA and it can be  
CC administered into a spray formulation via nasal cavity and thus its  
CC application is convenient for children. It is able to inhibit the  
CC growth of the wild-type virus and thus its therapeutic effect can be  
CC expected. The present sequence represents the influenza virus PB1  
CC protein gene.

XX SQ Sequence 2341 BP; 805 A; 461 C; 530 G; 545 T; 0 other;

Query Match 27.6%; Score 28.4; DB 20; Length 2341;  
Best Local Similarity 56.4%; Pred. No. 22;  
Matches 53; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

OY 10 GGAATACAGTTAATGACAGCATTAATAGCTCCTGCATATGTAATGCTAATACAGTT 69  
DB 2232 GAAGAGAGAGTCTGCTGAGATGATGAGATGCTGTCACCATTTAAGAGCTCAGACGCA 2291  
OY 70 AAAAAAACGGTATTTCCCTGCTTCTGATCCACA 103  
DB 2292 AAAATAGTGAATTTAGCTGTCTTCATGAAAA 2325

RESULT 18  
AA235351  
ID AA235351 standard; DNA; 41599 BP.

XX AC AA235351;  
XX 27-MAR-2000 (first entry)

DE Cosmid including sequence spanning human chromosome 9p21.  
XX  
XX Chromosome 9p21; human; cancer; tumour; diagnosis; prognosis;  
KW methylthioadenosine phosphorylase; glioma; melanoma;  
KW primary lymphoid malignancy; non-small cell lung cancer;  
KW head and neck cancer; ovarian cancer; bladder cancer;  
KW chondrosarcoma; ds.  
XX  
XX Homo sapiens.  
XX OS  
XX PN M09967634-A1.  
XX PD 29-DEC-1999.  
XX PF 21-JUN-1999; 99WC-US13981.  
XX PR 23-JUN-1998; 98US-0090411.  
XX PR 17-JUN-1999; 99US-0335231.  
XX (REGC ) UNIV CALIFORNIA.  
XX PA  
XX PI Carson DA, Schmid M, Carrera CJ;  
XX DR WPI; 2000-126650/11.  
XX  
XX Diagnosing and determining prognosis for cancer causatively associated  
PT with derangements of chromosome 9p21

XX PS Disclosure; Fig 7; 55pp; English.

CC This is the nucleotide sequence of a cosmid that includes sequences  
CC spanning human chromosome 9p21 (ATCC AC00047). This region  
CC harbours 5 genes within about 120 kb: the tumour suppressor genes  
CC p16INK4A (p15) with its alternatively spliced form p10, p16INK4A  
CC (p15) and p19ARF, and the gene for methylthioadenosine phosphorylase  
CC (MTHAP). The invention provides a method for diagnosis of, and  
CC determining a prognosis for, cancer causatively associated with  
CC derangements of chromosome 9p21. Underlying the invention is the  
CC discovery that such derangements have their geneis in deletions  
CC occurring centromeric to SRS 3.21, most often including breakpoints  
CC in exon 8 and/or between exons 4 and 5 of the gene which encodes  
CC MTHAP. As the cancer and tumour development advance, deletions in  
CC 9p21 progress centromerically from the geneis point toward the  
CC gene encoding p16. Thus, the method of the invention is performed  
CC by determining whether (a) portions of the 9p21 region including  
CC and telomeric to SRS 3.21 are deleted, and (b) portions of the  
CC 9p21 region centromeric to SRS 3.21 are deleted, where a positive  
CC finding in step (a) and a negative finding in step (b) are  
CC indicative of a cancer in an early stage of tumour development  
CC and a positive finding in step (a) is indicative of a cancer in an  
CC advanced stage of tumour development. Primer pairs (see AA235354-75)  
CC are provided for use in claimed methods for diagnosing and  
CC determining a prognosis for cancer associated with derangements of  
CC 9p21, especially a glioma, primary lymphoid malignancy, non-small  
CC cell lung cancer, melanoma, head and neck cancer, ovarian cancer,  
CC bladder cancer or a chondrosarcoma (claimed).

XX SQ Sequence 41599 BP; 13477 A; 8216 C; 8242 G; 11664 T; 0 other;

Query Match 27.6%; Score 28.4; DB 21; Length 41599;  
Best Local Similarity 58.1%; Pred. No. 38;  
Matches 50; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

OY 5 TGACTGGAATACAGTTAATGACAGCATTAATAGCTCCTGCATATGTAATGCTAATA 64  
DB 5850 TAAATGAAAAAAGTTAATTAATGTTTGTTCCTCCCTGCAAACTTAAAAACACACA 5909  
OY 65 CAGTTAAAAAAGGTATTTCCCTGG 90  
DB 5910 CACATTAATATCAGTGTCTTTCAGG 5935

RESULT 19  
AAH08436  
ID AAH08436 standard; cDNA; 804 BP.

XX AC AAH08436;  
XX 26-JUN-2001 (first entry)

DE Human cDNA clone (5'-primer) SEQ ID NO:5271.  
XX  
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.  
XX OS  
XX PN Homo sapiens.  
XX PD EP1074617-A2.  
XX PF 07-FEB-2001.  
XX PR 28-JUL-2000; 2000EP-0116126.  
XX PR 29-JUL-1999; 99JP-0248036.  
XX PR 27-AUG-1999; 99JP-0300253.  
XX PR 11-JAN-2000; 2000JP-0118776.  
XX PR 02-MAY-2000; 2000JP-0183767.  
XX PR 09-JUN-2000; 2000JP-0241899.  
XX  
XX (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
 XX  
 DR WPI: 2001-318749/34.  
 XX  
 PT Primer sets for synthesizing polynucleotides, particularly the 5602  
 PT full-length cDNAs defined in the specification, and for the detection  
 PT and/or diagnosis of the abnormality of the proteins encoded by the  
 PT full-length cDNAs -  
 XX  
 PS Claim 1: SEQ ID 5271: 2537pp + CD ROM; English.  
 XX  
 CC The present invention describes primer sets for synthesizing 5602  
 CC full-length cDNAs defined in the specification. Where a primer set  
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary  
 CC to the complementary strand of a polynucleotide which comprises one of  
 CC the 5602 nucleotide sequences defined in the specification, where the  
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 CC of an oligonucleotide comprising a sequence complementary to the  
 CC complementary strand of a polynucleotide which comprises a 5'-end  
 CC sequence and an oligonucleotide comprising a sequence complementary to a  
 CC polynucleotide which comprises a 3'-end sequence, where the  
 CC oligonucleotide comprises at least 15 nucleotides and the combination of  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in  
 CC the specification. The primer sets can be used in antisense therapy and  
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632  
 CC represent oligonucleotides, all of which are used in the exemplification  
 CC of the present invention.  
 CC  
 SQ Sequence 804 BP; 259 A; 170 C; 165 G; 207 T; 3 other;  
 XX  
 Query Match 27.4%; Score 28.2; DB 22; Length 804;  
 Best Local Similarity 61.6%; Pred. No. 21;  
 Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
 OY 13 ATACAGTTTAAAGCAGCATTAATAGCTCGCATATGTGAATTCCTAATACAGTTAA 72  
 DB 424 ACAACCTTTTAAGATATCATTAACACACATCCCTTGGGAATTTGGAACCGTTTAA 483  
 OY 73 AAACGGTATTTTC 85  
 DB 484 AGAGACACCTTTC 496  
 XX  
 RESULT 20  
 AAH18260  
 ID AAH18260 standard; cDNA: 2362 BP.  
 AC AAH18260;  
 XX  
 XX 26-JUN-2001 (first entry)  
 DT  
 XX Human cDNA sequence SEQ ID NO:18222.  
 DE  
 XX Human; primer: detection; diagnosis; antisense therapy; gene therapy; ss.  
 KM  
 XX Homo sapiens.  
 OS  
 XX  
 XX EP1074617-A2.  
 PN  
 XX 07-FEB-2001.  
 PD  
 XX 28-JUL-2000; 2000EP-0116126.  
 PF  
 XX 29-JUL-1999; 99JP-0248036.  
 PR 27-AUG-1999; 99JP-0300253.  
 PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.  
 PR 09-JUN-2000; 2000JP-0241899.  
 XX  
 PA (HELI-) HELIX RES INST.  
 XX  
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
 XX  
 DR WPI: 2001-318749/34.  
 XX  
 PT Primer sets for synthesizing polynucleotides, particularly the 5602  
 PT full-length cDNAs defined in the specification, and for the detection  
 PT and/or diagnosis of the abnormality of the proteins encoded by the  
 PT full-length cDNAs -  
 XX  
 PS Claim 8: SEQ ID 18222; 2537pp + CD ROM; English.  
 XX  
 CC The present invention describes primer sets for synthesizing 5602  
 CC full-length cDNAs defined in the specification. Where a primer set  
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary  
 CC to the complementary strand of a polynucleotide which comprises one of  
 CC the 5602 nucleotide sequences defined in the specification, where the  
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 CC of an oligonucleotide comprising a sequence complementary to the  
 CC complementary strand of a polynucleotide which comprises a 5'-end  
 CC sequence and an oligonucleotide comprising a sequence complementary to a  
 CC polynucleotide which comprises a 3'-end sequence, where the  
 CC oligonucleotide comprises at least 15 nucleotides and the combination of  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in  
 CC the specification. The primer sets can be used in antisense therapy and  
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632  
 CC represent oligonucleotides, all of which are used in the exemplification  
 CC of the present invention.  
 CC  
 SQ Sequence 2362 BP; 659 A; 512 C; 562 G; 629 T; 0 other;  
 XX  
 Query Match 27.4%; Score 28.2; DB 22; Length 2362;  
 Best Local Similarity 61.6%; Pred. No. 25;  
 Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
 OY 13 ATACAGTTTAAAGCAGCATTAATAGCTCGCATATGTGAATTCCTAATACAGTTAA 72  
 DB 424 ACAACCTTTTAAGATATCATTAACACACATCCCTTGGGAATTTGGAACCGTTTAA 483  
 OY 73 AAACGGTATTTTC 85  
 DB 484 AGAGACACCTTTC 496  
 XX  
 RESULT 21  
 AA243957  
 ID AA243957 standard; cDNA: 3002 BP.  
 AC AA243957;  
 XX  
 XX 17-MAR-2000 (first entry)  
 DT  
 XX Human DAN cDNA.  
 DE  
 XX  
 XX DAN: deadenylating nuclease; cytostatic; immunosuppressor; human;  
 KM neuropeptide; anti-inflammatory; cancer; autoimmune disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 58..1977  
 FT /\*tag= a

FT XX /product- "DAN"  
PN MO9958647-A2.  
XX 18-NOV-1999.  
PD 05-MAY-1999: 99WO-EP03071.  
PF 08-MAY-1998: 98DE-1022122.  
XX  
XX (AVERT ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.  
PA Huelts C, Gallert K, Koerner C, Wahle E;  
XX WPI: 2000-072335/06.  
DR DNA encoding a human deadenylation nuclease, used to, e.g. treat  
PT Alzheimer's disease -  
XX  
XX Claim 3: Page 39-40; 46pp; German.  
PS  
XX This invention describes a novel nucleic acid (I) encoding a human  
CC deadenylation nuclease (DAN) which has cytosolic, immunosuppressive,  
CC neuroprotective and anti-inflammatory activity. (I) can be used to  
CC identify functional interactors, to identify and isolate human variants  
CC from Genbank or to treat or diagnose cancer, autoimmune disease, in  
CC particular multiple sclerosis or rheumatoid arthritis, Alzheimer's  
CC disease, allergies, especially neurodermatitis, Type I or IV allergies,  
CC arthrosis, atherosclerosis, osteoporosis, acute and chronic infections  
CC and/or diabetes and/or influencing cell metabolism, in particular  
CC immunosuppression for transplantation. This sequence encodes a human DAN  
CC protein which is described in the method of the invention.  
XX  
SQ Sequence 3002 BP; 869 A; 633 C; 703 G; 797 T; 0 other;  
Query Match 27.4%; Score 28.2; DB 21; Length 3002;  
Best Local Similarity 61.6%; Pred. No. 27;  
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
QY 13 ATACAGCTTTAATGACAGCATTAATAGCTCCGATATGTAATGCTAATACAGTTAA 72  
DB 1050 ACAACCTTTTAAGGATATCATTAACAACACATCCCTTGCGAATTTGGAACGCGTTAA 1109  
QY 73 AAAACGSTATTTTC 85  
DB 1110 ACAGACACCTTTTC 1122  
DE Human dltlp nucleic acid synthesis/modification protein-encoding cDNA.  
XX  
XX Human: dltlp; diagnostic and therapeutic polynucleotide; diagnosis;  
KW cancer; cell proliferative disorder; autoimmune disorder;  
KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;  
KW neurological disorder; gastrointestinal disorder; transport disorder;  
KW connective tissue disorder; drug screening; proteome analysis;  
KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;  
KW disease model; toxicological testing; transcript imaging;  
KW nucleic acid synthesis; nucleic acid modification; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200297031-A2.  
XX  
PD 05-DEC-2002.  
XX

PF 27-MAR-2002; 2002WO-US10056.  
XX  
PR 28-MAR-2001; 2001US-279619P.  
PR 29-MAR-2001; 2001US-280067P.  
PR 29-MAR-2001; 2001US-280068P.  
PR 16-MAY-2001; 2001US-291280P.  
PR 17-MAY-2001; 2001US-291829P.  
PR 17-MAY-2001; 2001US-291849P.  
PR 19-JUN-2001; 2001US-299428P.  
PR 20-JUN-2001; 2001US-299776P.  
PR 20-JUN-2001; 2001US-300001P.  
XX  
PA (INCY- ) INCYTE GENOMICS INC.  
XX  
XX Dafio A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
PI Dufour GE, Hillman JL, Yu JY, Tnason O, Yap PE, Amshay SR;  
PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleeefeld Y, Gerstlin EH;  
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
PI Flores V, Marwaha R, Lo A, Lan RV, Urashka ME;  
XX  
XX WPI: 2003-129518/12.  
DR P-PsDB; ABR41545.  
DR  
XX  
XX Novel human diagnostic and therapeutic polypeptide useful for  
PT identifying test compound which specifically binds to a polypeptide  
PT encoded by human diagnostic and therapeutic polynucleotide, and to  
PT induce antibodies -  
XX  
PS Claim 2; SEQ ID No 404; 591pp; English.  
XX  
XX The invention relates to novel human diagnostic and therapeutic  
CC polynucleotides designated dltlp (ACC46080-ACC46749) and to their  
CC encoded proteins (DTRP; ABR41136-ABR41812). The invention also relates  
CC to polynucleotide sequences at least 90% identical to the dltlp cDNA  
CC sequences of the invention; recombinant vectors, host cells and  
CC transgenic organisms comprising a dltlp nucleic acid sequence; the  
CC recombinant production of DTRP proteins; antibodies specific for DTRP  
CC proteins; microarrays comprising dltlp nucleic acid sequences; methods  
CC of detecting dltlp nucleotide and protein sequences; methods of screening  
CC for compounds which specifically bind a DTRP protein; and methods of  
CC assessing the toxicity of test compounds using a dltlp hybridisation  
CC probe. Dltlp nucleic acid sequences and DTRP proteins may be used in the  
CC diagnosis of a wide variety of conditions including cancer and other cell  
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,  
CC viral, fungal or parasitic infections; hormonal disorders; metabolic  
CC disorders; neurological disorders; gastrointestinal disorders; transport  
CC disorders; and connective tissue disorders. They may also be used to  
CC screen for modulators of protein activity or gene expression. DTRP  
CC proteins can additionally be used in analysis of the proteome of a tissue  
CC or cell type and to induce antibodies. The dltlp nucleic acids are  
CC additionally useful in somatic or germline gene therapy of the disorders  
CC mentioned above, as a source of antisense sequences, as a source of  
CC probes and primers, in genotyping and identification of individuals, in  
CC the generation of transgenic animal models of human disease or knock in  
CC humanised animals, in toxicological testing, and in transcript imaging.  
CC The present sequence represents a dltlp cDNA encoding a DTRP protein  
CC which is involved in nucleic acid synthesis and/or modification.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 3073 BP; 861 A; 662 C; 735 G; 815 T; 0 other;  
Query Match 27.4%; Score 28.2; DB 25; Length 3073;  
Best Local Similarity 61.6%; Pred. No. 27;  
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
QY 13 ATACAGCTTTAATGACAGCATTAATAGCTCCGATATGTAATGCTAATACAGTTAA 72  
DB 1133 ACAACCTTTTAAGGATATCATTAACAACACATCCCTTGCGAATTTGGAACGCGTTAA 1192  
QY 73 AAAACGSTATTTTC 85  
DB 1110 ACAGACACCTTTTC 1122

Db 1193 AGAGACACTTTC 1205

RESULT 23  
AAK51618  
ID AAK51618 standard; cDNA; 3078 BP.

XX AAK51618;  
AC AAK51618;  
XX  
XX  
DT 06-NOV-2001 (first entry)  
XX  
XX Human polynucleotide SEQ ID NO 163.  
DE  
XX  
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorder; arthritis; inflammation; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200157190-A2.  
PN  
XX  
XX 09-AUG-2001.  
PD  
XX  
XX 05-FEB-2001; 2001WO-US04098.  
PF  
XX  
XX 03-FEB-2000; 2000US-0496914.  
PR 27-APR-2000; 2000US-0560875.  
PR 20-JUN-2000; 2000US-0598075.  
PR 19-JUL-2000; 2000US-0620325.  
PR 01-SEP-2000; 2000US-0654936.  
PR 15-SEP-2000; 2000US-0663561.  
PR 20-OCT-2000; 2000US-0693325.  
PR 30-NOV-2000; 2000US-0728422.  
XX  
XX (HYSE-) HYSEQ INC.  
PA  
XX  
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;  
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;  
XX  
XX WPI: 2001-476283/51.  
DR P-PSDB: AAM78485.  
XX  
XX Nucleic acids encoding polypeptides with cytokine-like activities,  
PT useful in diagnosis and gene therapy -  
XX  
XX Claim 1: Page 886-889; 6221pp; English.  
PS  
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation.  
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
CC (AAM80020) are omitted as the relevant pages from the sequence listing  
CC were missing at the time of publication.  
XX  
XX Sequence 3078 BP; 873 A; 664 C; 729 G; 812 T; 0 other;

Query Match 27.4%; Score 28.2; DB 22; Length 3078;  
Best Local Similarity 61.6%; Pred. No. 27;  
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

0Y 13 ATACAGCTTAATGACAGATTAAAGCTCTGCATATGTAATTCGTAATACAGTTAAA 72  
Db 1133 ACAACCTTTAAAGGATATCAATTAACAACATCCCTGCGAATTGGAAGGCGGTTAAA 1192

QY 73 AAACGGTATTTTC 85  
Db 1193 AGAGACACTTTC 1205

RESULT 24  
AAK52602  
ID AAK52602 standard; cDNA; 3086 BP.

XX AAK52602;  
AC AAK52602;  
XX  
XX  
DT 06-NOV-2001 (first entry)  
XX  
XX Human polynucleotide SEQ ID NO 2131.  
DE  
XX  
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorder; arthritis; inflammation; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200157190-A2.  
PN  
XX  
XX 09-AUG-2001.  
PD  
XX  
XX 05-FEB-2001; 2001WO-US04098.  
PF  
XX  
XX 03-FEB-2000; 2000US-0496914.  
PR 27-APR-2000; 2000US-0560875.  
PR 20-JUN-2000; 2000US-0598075.  
PR 19-JUL-2000; 2000US-0620325.  
PR 01-SEP-2000; 2000US-0654936.  
PR 15-SEP-2000; 2000US-0663561.  
PR 20-OCT-2000; 2000US-0693325.  
PR 30-NOV-2000; 2000US-0728422.  
XX  
XX (HYSE-) HYSEQ INC.  
PA  
XX  
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;  
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;  
XX  
XX WPI: 2001-476283/51.  
DR P-PSDB: AAM79469.  
XX  
XX Nucleic acids encoding polypeptides with cytokine-like activities,  
PT useful in diagnosis and gene therapy -  
XX  
XX Claim 1: Page 4503-4504; 6221pp; English.  
PS  
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation.  
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
CC (AAM80020) are omitted as the relevant pages from the sequence listing  
CC were missing at the time of publication.  
XX  
XX Sequence 3086 BP; 873 A; 668 C; 729 G; 815 T; 1 other;

Query Match 27.4%; Score 28.2; DB 22; Length 3086;  
Best Local Similarity 61.6%; Pred. No. 27;  
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;



PR 18-AUG-1998: 98US-0096950.  
PR 18-AUG-1998: 98US-0096959.  
PR 18-AUG-1998: 98US-0096960.  
PR 18-AUG-1998: 98US-0097022.  
PR 19-AUG-1998: 98US-0097141.  
PR 20-AUG-1998: 98US-0097218.  
PR 24-AUG-1998: 98US-0097661.  
PR 26-AUG-1998: 98US-0097951.  
PR 26-AUG-1998: 98US-0097952.  
PR 26-AUG-1998: 98US-0097954.  
PR 26-AUG-1998: 98US-0097955.  
PR 26-AUG-1998: 98US-0097971.  
PR 26-AUG-1998: 98US-0097974.  
PR 26-AUG-1998: 98US-0097978.  
PR 26-AUG-1998: 98US-0097979.  
PR 26-AUG-1998: 98US-0097986.  
PR 26-AUG-1998: 98US-0098014.  
PR 31-AUG-1998: 98US-0098525.  
PR 16-SEP-1998: 98US-0100634.  
PR 12-JAN-1999: 99US-0115565.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
PI Wood WI, Yuan J;  
XX  
XX WPI: 2000-072883/06.  
XX  
XX Membrane-bound proteins and related nucleotide sequences -  
XX  
XX Examples: Fig 60: 822pp: English.  
XX  
XX The invention provides membrane-bound PRO polypeptides and  
XX polynucleotides encoding them. The PRO sequences of the invention were  
XX identified based on extracellular domain homology screening. The PRO  
XX sequences have homology with proteins including LDL receptors, TIE  
XX ligands and various enzymes. The membrane-bound proteins and receptor  
XX molecules are useful as pharmaceutical and diagnostic agents. Receptor  
XX immunoadhesins, for instance, can be used as therapeutic agents to block  
XX receptor-ligand interactions. The membrane-bound proteins can also be  
XX employed for screening of potential peptide or small molecule inhibitors  
XX of the relevant receptor/ligand interaction. The PRO encoding sequences  
XX are useful as hybridization probes, in chromosome and gene mapping and in  
XX the generation of antisense RNA and DNA. PRO nucleic acid sequences  
XX will also be useful for the preparation of PRO polypeptides, especially  
XX by recombinant techniques.  
XX  
XX Sequence 466 BP; 116 A; 77 C; 115 G; 149 T; 9 other:  
XX  
XX Query Match 27.2%; Score 28; DB 21; Length 466;  
XX Best Local Similarity 59.7%; Pred. No. 21;  
XX Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
KW diagnostic assay; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200073454-A1.  
XX  
XX PD 07-DEC-2000.  
XX  
XX 30-MAR-2000; 2000WO-US08439.  
XX  
XX 02-JUN-1999: 99WO-US12252.  
XX 23-JUN-1999: 99US-0141037.  
XX 07-JUL-1999: 99US-0143048.  
XX 20-JUL-1999: 99US-0144758.  
XX 26-JUL-1999: 99US-0145698.  
XX 28-JUL-1999: 99US-0146222.  
XX 17-AUG-1999: 99US-0149396.  
XX 15-SEP-1999: 99WO-US21090.  
XX 15-SEP-1999: 99WO-US21547.  
XX 08-OCT-1999: 99US-0158663.  
XX 30-NOV-1999: 99WO-US28313.  
XX 01-DEC-1999: 99WO-US28301.  
XX 16-DEC-1999: 99WO-US30095.  
XX 20-DEC-1999: 99WO-US30911.  
XX 05-JAN-2000: 2000WO-US00219.  
XX 06-JAN-2000: 2000WO-US00376.  
XX 11-FEB-2000: 2000WO-US03565.  
XX 18-FEB-2000: 2000WO-US04341.  
XX 22-FEB-2000: 2000WO-US04414.  
XX 24-FEB-2000: 2000WO-US04914.  
XX 24-FEB-2000: 2000WO-US05004.  
XX 02-MAR-2000: 2000WO-US05841.  
XX 15-MAR-2000: 2000WO-US06884.  
XX 20-MAR-2000: 2000WO-US07377.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
XX Grimaldi CJ, Gurney AL, Kijavyn IJ, Napier MA, Pan J, Peoni NF;  
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
XX Zhang Z;  
XX  
XX WPI: 2001-032160/04.  
XX  
XX PRO polynucleotides used to produce polypeptides used to target  
XX bioactive molecules such as toxins, radiolabels or antibodies, to  
XX specific cells, to cause targeted cell death -  
XX  
XX Example 25: Fig 60: 935pp: English.  
XX  
XX The present invention describes human secreted and transmembrane PRO  
XX proteins. The PRO proteins have cytostatic activity. The PRO proteins  
XX can be used for targeted delivery of bioactive molecules, such as  
XX toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
XX sequences, and their fragments, can be used as hybridisation probes. In  
XX chromosomes and gene mapping, and in the generation of anti-sense RNA  
XX and DNA. They may also be used to produce transgenic animals which are  
XX used to develop and screen therapeutically useful reagents. The PRO  
XX nucleotide and protein sequence can be used for tissue typing and in  
XX treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
XX AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
XX in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
XX AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
XX sequences given in the exemplification of the present invention.  
XX  
XX Sequence 466 BP; 116 A; 77 C; 115 G; 149 T; 9 other:  
XX  
XX Query Match 27.2%; Score 28; DB 22; Length 466;  
XX Best Local Similarity 59.7%; Pred. No. 21;  
XX Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 5 TGACTGGAATACAGTTTAATGACAGATTATAGTCCTGATGTAATGCTTATA 64  
||| ||| | | ||| ||| | ||| ||| | | | | |  
Db 216 TGAGTGGTTTAAATCTTTCATGCTGGGATAAATACAGCTGATATGATATCCACCA 157  
QY 65 CAGTTAAAAAACCGTA 81  
| | | | | | | | | |  
Db 156 CCCGTAAAAAATAGTA 140

RESULT 27  
ABX80189/c  
ID ABX80189 standard; DNA: 466 BP.  
XX  
AC ABX80189;  
XX  
DT 28-APR-2003 (first entry)  
XX  
De Novel human secreted or transmembrane protein related DNA28357.  
XX  
KW Human; PRO: hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpesiformis; Crohn's disease; chondrocyte differentiation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN US2002132252-A1.  
XX  
PD 19-SEP-2002.  
XX  
PF 14-NOV-2001; 2001US-0990442.  
XX  
PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 06-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 02-MAR-2000; 2000WO-US05004.  
PR 10-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06319.  
PR 20-MAR-2000; 2000WO-US06884.  
PR 30-MAR-2000; 2000WO-US07377.  
PR 15-MAY-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13358.  
PR 22-MAY-2000; 2000WO-US13705.  
PR 30-MAY-2000; 2000WO-US14042.  
PR 02-JUN-2000; 2000WO-US14941.  
PR 28-JUL-2000; 2000WO-US15264.  
PR 11-AUG-2000; 2000WO-US20710.  
PR 23-AUG-2000; 2000WO-US22031.  
PR

PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-0478787.  
PR 17-OCT-1997; 97US-0622508.  
PR 12-NOV-1997; 97US-0651866.  
PR 13-NOV-1997; 97US-0653116.  
PR 24-NOV-1997; 97US-0667709.  
PR 25-FEB-1998; 98US-0759456.  
PR 20-MAR-1998; 98US-0789106.  
PR 28-APR-1998; 98US-0833226.  
PR 07-MAY-1998; 98US-0846006.  
PR 28-MAY-1998; 98US-0871066.  
PR 02-JUN-1998; 98US-0876097.  
PR 02-JUN-1998; 98US-0877599.  
PR 03-JUN-1998; 98US-0878276.  
PR 04-JUN-1998; 98US-0880216.  
PR 04-JUN-1998; 98US-0880256.  
PR 04-JUN-1998; 98US-0880266.  
PR 04-JUN-1998; 98US-0880286.  
PR 04-JUN-1998; 98US-0880296.  
PR 04-JUN-1998; 98US-0880306.  
PR 04-JUN-1998; 98US-0880336.  
PR 04-JUN-1998; 98US-0883266.  
PR 05-JUN-1998; 98US-0881676.  
PR 05-JUN-1998; 98US-0882026.  
PR 05-JUN-1998; 98US-0882126.  
PR 05-JUN-1998; 98US-0882176.  
PR 09-JUN-1998; 98US-0886556.  
PR 10-JUN-1998; 98US-0887346.  
PR 10-JUN-1998; 98US-0887386.  
PR 10-JUN-1998; 98US-0887426.  
PR 10-JUN-1998; 98US-0888106.  
PR 10-JUN-1998; 98US-0888246.  
PR 10-JUN-1998; 98US-0888266.  
PR 11-JUN-1998; 98US-0888586.  
PR 11-JUN-1998; 98US-0888616.  
PR 11-JUN-1998; 98US-0888766.  
PR 12-JUN-1998; 98US-0891056.  
PR 16-JUN-1998; 98US-0894406.  
PR 16-JUN-1998; 98US-0895126.  
PR 16-JUN-1998; 98US-0895146.  
PR 17-JUN-1998; 98US-0895326.  
PR 17-JUN-1998; 98US-0895386.  
PR 17-JUN-1998; 98US-0895986.  
PR 17-JUN-1998; 98US-0895996.  
PR 17-JUN-1998; 98US-0896006.  
PR 17-JUN-1998; 98US-0896536.  
PR 18-JUN-1998; 98US-0898016.  
PR 18-JUN-1998; 98US-0898076.  
PR 18-JUN-1998; 98US-0899086.  
PR 28-AUG-2001; 2001US-0941992.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX  
DR WPI, 2003-247083/24.  
XX  
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
PT are therapeutically useful for enhancing immune response and in cancer  
PT treatments

XX Disclosure: Fig 61; 648bp; English.  
PS The invention describes an isolated human PRO polypeptide. The PRO  
XX polypeptides are useful in detecting PRO polypeptides in a sample, in  
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
CC in modulating at least one biological activity of a cell expressing a PRO  
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
CC useful for treating cardiac insufficiency disorders. PRO154 and PRO186  
CC stimulate adrenal cortical insufficiency disorders. PRO154 and PRO186  
CC PRO1943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
CC useful for treating conditions or disorders where angiogenesis must be  
CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
CC useful for treating cancers tumours. PRO812 inhibits vascular  
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
CC cells and is thus useful for inhibiting endothelial cell growth in  
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
CC immune response. PRO828, PRO1068 or PRO1132 enhance survival of  
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
CC rod photoreceptor cells) and therefore are useful for treating retinal  
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813  
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,  
CC and therefore are useful for treating kidney disorders associated with  
CC decreased mesangial cell function such as Berger disease or other  
CC nephropathies associated with dermatitis, herpetic disease or Crohn's  
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
CC proliferation and/or redifferentiation of chondrocytes in culture and  
CC are thus useful for treating sports injuries, and arthritis. This  
CC sequence represents a novel human PRO protein polynucleotide.  
SQ Sequence 466 BP; 116 A; 77 C; 115 G; 149 T; 9 other:  
Query Match 27.2%; Score 28; DB 25; Length 466;  
Best Local Similarity 59.7%; Pred. No. 21;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
QY 5 TGACGTGAGTAACAGTTTATGACAGATTATAGCTCGATGATGTAATTCGTAATA 64  
DB 216 TGAGTGCTTNAATCTTCATGCTGGATTAATACAGCTGATCATATATATCCACCA 157  
QY 65 CAGTTAAAAAAGGTA 81  
DB 156 CCCTGTAAAAAATAGTA 140  
RESUR 28  
ABX80693/c  
ID ABX80693 standard; CDNA; 466 BP.  
AC ABX80693;  
XX  
XX 22-APR-2003 (first entry)  
DT  
XX  
DE Human secreted/transmembrane protein CDNA, #38.  
XX  
XX Human: gene; ss: PRO; secreted; transmembrane; pharmaceutical;  
KW diagnostic; biosensor; bioreactor; tumour; therapeutic;  
KW gene therapy; tumour-associated antigenic target; TAT; ADPP;  
KW antibody-dependent enzyme mediated prodrg therapy; cytosstatic.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US2003027162-A1.  
PN  
XX  
PD 06-FEB-2003.  
XX  
XX 15-NOV-2001; 2001US-0997428.  
PF  
XX 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1996; 98WO-US19330.

PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 02-MAR-2000; 2000WO-US05004.  
PR 10-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06319.  
PR 20-MAR-2000; 2000WO-US06884.  
PR 30-MAR-2000; 2000WO-US07377.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.  
PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088336P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.





XX 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 02-MAR-2000; 2000WO-US05004.  
PR 10-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06319.  
PR 20-MAR-2000; 2000WO-US06884.  
PR 30-MAR-2000; 2000WO-US07377.  
PR 15-MAY-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13358.  
PR 22-MAY-2000; 2000WO-US13705.  
PR 30-MAY-2000; 2000WO-US14042.  
PR 02-JUN-2000; 2000WO-US14941.  
PR 28-JUL-2000; 2000WO-US15264.  
PR 11-AUG-2000; 2000WO-US20710.  
PR 23-AUG-2000; 2000WO-US22031.  
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QY 65 CAGCTAAAAAACGGA 81  
DB 156 CCCTGTAATAAATAGTA 140

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AC ABX90166;  
XX  
DT 01-MAY-2003 (first entry)  
XX  
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XX  
KW Human; gene; ss; PRO; secreted; transmembrane; signal peptide;  
KW pharmaceutical; diagnostic; therapeutic; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN US2002160384-A1.  
XX  
PD 31-OCT-2002.  
XX  
PE 14-NOV-2001; 2001US-0992598.  
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PR 15-SEP-1999; 99WO-US21547.

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PR 20-MAR-1998; 98US-078910P.  
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PR 28-AUG-2001: 2001US-0941992.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX  
DR WPI: 2003-288106/28.  
XX  
PT New transmembrane polypeptides and nucleic acids encoding the  
PT polypeptides, useful in gene therapy, in chromosome identification, as  
PT chromosome markers, or in generating probes -  
XX  
PS Example 25; Fig 60; 650pp; English.  
XX  
CC The invention discloses isolated PRO secreted/transmembrane polypeptides  
CC comprising a sequence without signal peptide and the nucleic acid  
CC encoding them. The polypeptides can be used to raise antibodies that  
CC specifically bind to the PRO polypeptide, for linking a bioactive  
CC molecule to a cell expressing a PRO protein and for modulating at least  
CC one biological activity of a cell. The PRO polypeptides or  
CC polynucleotides are also useful in gene therapy, in chromosome  
CC identification, as chromosome markers, or in generating probes. The PRO  
CC polypeptides are useful as molecular markers for protein  
CC electrophoresis, and the isolated nucleic acids may be used for  
CC recombinantly expressing those markers. The PRO polypeptides and nucleic  
CC acids may also be used in tissue typing. Anti-PRO antibodies are useful  
CC in diagnostic assays for PRO, and in affinity purification of PRO from  
CC recombinant cell culture or natural sources. The sequences presented in  
CC ABX90083-ABX90468 are the genes encoding, the primers amplifying and the  
CC probes detecting the PRO polynucleotides of the invention.  
CC Note: The sequence data for this patent is also available in electronic  
CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
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Best Local Similarity 59.7%; Pred. No. 21;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
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AC ABX77777;  
XX  
DT 14-APR-2003 (first entry)  
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KW Human: PRO; gene; ss; cytosolic; tumour; cancer; breast; lung; stomach;  
KW liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;  
KW

KW antibody-dependent enzyme mediated prodrug therapy.  
OS Homo sapiens.  
XX  
PN US2003027163-A1.  
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PD 06-FEB-2003.  
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PR 17-AUG-1998; 98US-096766P.
PR 17-AUG-1998; 98US-096768P.
PR 17-AUG-1998; 98US-096773P.
PR 17-AUG-1998; 98US-096791P.
PR 17-AUG-1998; 98US-096867P.
PR 17-AUG-1998; 98US-096891P.
PR 17-AUG-1998; 98US-096894P.
PR 17-AUG-1998; 98US-096895P.
PR 17-AUG-1998; 98US-096897P.
PR 18-AUG-1998; 98US-096949P.
PR 18-AUG-1998; 98US-096950P.
PR 18-AUG-1998; 98US-096953P.
PR 18-AUG-1998; 98US-096960P.
PR 18-AUG-1998; 98US-097022P.
PR 19-AUG-1998; 98US-097141P.
PR 20-AUG-1998; 98US-097218P.
PR 24-AUG-1998; 98US-097611P.
PR 26-AUG-1998; 98US-097952P.
PR 26-AUG-1998; 98US-097954P.
PR 26-AUG-1998; 98US-097955P.
PR 26-AUG-1998; 98US-097971P.
PR 26-AUG-1998; 98US-097974P.
PR 26-AUG-1998; 98US-097978P.
PR 26-AUG-1998; 98US-097979P.
PR 26-AUG-1998; 98US-097986P.
PR 26-AUG-1998; 98US-098014P.
PR 31-AUG-1998; 98US-098525P.
PR 16-SEP-1998; 98US-100634P.
PR 17-SEP-1998; 98US-100838P.
PR 22-DEC-1998; 98US-113296P.
PR 12-MAR-1999; 98US-123957P.
PR 23-JUN-1999; 98US-141037P.
PR 07-JUL-1999; 98US-143048P.

Query Match 27.2%; Score 28; DB 25; Length 466;
Best Local Similarity 59.7%; Pred. No. 21;
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 5 TGACTGCAATTAACGTTAATGACAGCATTTAATAGCTCCATCATGTGTAATGCTATA 64
    ||| ||| || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 216 TGAGTGGTTNAATCTTATGATGGGATAAATAACAGCTCATCTATGATTAATCCACA 157
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 65 CAGTTAAAAAAGGTA 81
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 156 CCTGTAAAAAATAGTA 140
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 32.
ABX79373/c
ID ABX79373 standard; cDNA; 466 BP.
XX ABX79373;
AC 17-APR-2003 (first entry)
XX
XX Human secreted/transmembrane protein cDNA, #38.
DE
XX
XX Human; gene; ss; PRO; secreted; transmembrane; signal peptide;
KW pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic;
KW colon cancer; lung cancer; breast cancer;cancer; gene therapy.
XX
OS Homo sapiens.
```

```
XX  US2002142961-A1.
PN
PD  03-OCT-2002.
XX
XX  19-NOV-2001; 2001US-0989721.
PE
XX  05-NOV-1997; 97WO-US20069.
PR  17-SEP-1998; 98WO-US19437.
PR  07-OCT-1998; 98WO-US21141.
PR  01-DEC-1998; 98WO-US25108.
PR  05-JAN-1999; 99WO-US00106.
PR  08-MAR-1999; 99WO-US05028.
PR  02-JUN-1999; 99WO-US12252.
PR  15-SEP-1999; 99WO-US21090.
PR  15-SEP-1999; 99WO-US21547.
PR  30-NOV-1999; 99WO-US28313.
PR  01-DEC-1999; 99WO-US28301.
PR  16-DEC-1999; 99WO-US28634.
PR  20-DEC-1999; 99WO-US30095.
PR  05-JAN-2000; 2000WO-US00219.
PR  06-JAN-2000; 2000WO-US00376.
PR  11-FEB-2000; 2000WO-US03565.
PR  18-FEB-2000; 2000WO-US04341.
PR  22-FEB-2000; 2000WO-US04414.
PR  24-FEB-2000; 2000WO-US04914.
PR  02-MAR-2000; 2000WO-US05004.
PR  10-MAR-2000; 2000WO-US05841.
PR  15-MAR-2000; 2000WO-US06884.
PR  20-MAR-2000; 2000WO-US07377.
PR  30-MAR-2000; 2000WO-US08439.
PR  15-MAY-2000; 2000WO-US13358.
PR  17-MAY-2000; 2000WO-US14042.
PR  22-MAY-2000; 2000WO-US14941.
PR  02-JUN-2000; 2000WO-US15264.
PR  28-JUL-2000; 2000WO-US20710.
PR  11-AUG-2000; 2000WO-US22031.
PR  23-AUG-2000; 2000WO-US23522.
PR  24-AUG-2000; 2000WO-US23328.
PR  08-NOV-2000; 2000WO-US30952.
PR  01-DEC-2000; 2000WO-US32678.
PR  28-FEB-2001; 2001WO-US06520.
PR  01-JUN-2001; 2001WO-US17800.
PR  20-JUN-2001; 2001WO-US19692.
PR  29-JUN-2001; 2001WO-US21066.
PR  09-JUL-2001; 2001WO-US21735.
PR  16-JUN-1997; 97US-049787P.
PR  17-OCT-1997; 97US-062250P.
PR  12-NOV-1997; 97US-065186P.
PR  13-NOV-1997; 97US-065311P.
PR  24-NOV-1997; 97US-066770P.
PR  25-FEB-1998; 98US-075945P.
PR  20-MAR-1998; 98US-078910P.
PR  28-APR-1998; 98US-083322P.
PR  07-MAY-1998; 98US-084600P.
PR  28-MAY-1998; 98US-087106P.
PR  02-JUN-1998; 98US-087607P.
PR  02-JUN-1998; 98US-087609P.
PR  02-JUN-1998; 98US-087759P.
PR  03-JUN-1998; 98US-087827P.
PR  04-JUN-1998; 98US-088021P.
PR  04-JUN-1998; 98US-088025P.
PR  04-JUN-1998; 98US-088026P.
PR  04-JUN-1998; 98US-088028P.
PR  04-JUN-1998; 98US-088029P.
PR  04-JUN-1998; 98US-088030P.
PR  04-JUN-1998; 98US-088033P.
PR  04-JUN-1998; 98US-088326P.
PR  05-JUN-1998; 98US-088167P.
PR  05-JUN-1998; 98US-088202P.
XX
XX  05-JUN-1998; 98US-088212P.
PR  05-JUN-1998; 98US-088217P.
PR  09-JUN-1998; 98US-088655P.
PR  10-JUN-1998; 98US-088734P.
PR  10-JUN-1998; 98US-088738P.
PR  10-JUN-1998; 98US-088742P.
PR  10-JUN-1998; 98US-088810P.
PR  10-JUN-1998; 98US-088824P.
PR  10-JUN-1998; 98US-088826P.
PR  11-JUN-1998; 98US-088858P.
PR  11-JUN-1998; 98US-088861P.
PR  11-JUN-1998; 98US-088867P.
PR  12-JUN-1998; 98US-089105P.
PR  16-JUN-1998; 98US-089440P.
PR  16-JUN-1998; 98US-089512P.
PR  16-JUN-1998; 98US-089514P.
PR  17-JUN-1998; 98US-089532P.
PR  17-JUN-1998; 98US-089538P.
PR  17-JUN-1998; 98US-089588P.
PR  17-JUN-1998; 98US-089599P.
PR  17-JUN-1998; 98US-089600P.
PR  18-JUN-1998; 98US-089653P.
PR  18-JUN-1998; 98US-089801P.
PR  18-JUN-1998; 98US-089907P.
PR  18-JUN-1998; 98US-089908P.
PR  28-AUG-2001; 2001US-0941992.
XX
XX  (GETH ) GENENTECH INC.
XX
XX  Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DI,
PI  Ferrara N, Fong S, Gether H, Gerritsen ME, Goddard A, Godowski PJ,
PI  Grimaldi JC, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF,
PI  Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
PI  Zhang Z;
XX
XX  WPI; 2003-155950/15.
XX
XX  New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,
PT  PRO361 or PRO846) useful as targets for therapeutic intervention in
PT  cancers (e.g. lung or breast cancers), or for diagnosing these cancers
PT
XX
XX  Example 25; Fig 60; 647pp; English.
XX
XX  The invention discloses isolated PRO secreted/transmembrane polypeptides
CC  comprising a sequence without signal peptide and the nucleic acid
CC  encoding them. The polypeptides can be used to raise antibodies that
CC  specifically bind to the PRO polypeptide, for linking a bioactive
CC  molecule to a cell expressing a PRO protein and for modulating at least
CC  one biological activity of a cell. The PRO polypeptides or
CC  polynucleotides are also useful as pharmaceuticals, diagnostics,
CC  biosensors or bioreactors, for detecting or treating e.g. tumours in
CC  mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or
CC  rabbits as targets for therapeutic intervention in certain cancers (e.g.
CC  colon, lung or breast cancers) and diagnostic determination of the
CC  presence of these cancers. The PRO polypeptides are also useful as
CC  molecular weight markers or for chromosome identification. The PRO genes
CC  are useful as hybridisation probes or for screening libraries of human
CC  cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
CC  therapy, particularly for replacing a defective gene. The sequences
CC  presented in ABX79290-ABX79675 are the genes encoding, the primers
CC  amplifying and the probes detecting the PRO polynucleotides of the
CC  invention.
CC  Note: The sequence data for this patent is also available in electronic
CC  format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX  Sequence 466 BP; 116 A; 77 C; 115 G; 149 T; 9 other;
SQ
XX
XX  Query Match 27.2%; Score 28; DB 25; Length 466;
XX  Best Local Similarity 59.7%; Pred. No. 21;
XX  Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
```

5 TGACGTGGAATACAGCTTTAATGACAGCATTAATAGCTCCTGCAATATGTAATTGCTAATA 64



CC polypeptides, and for identifying agonists or antagonists.  
CC The polynucleotide sequences encoding PRO polypeptides are useful as  
CC hybridisation probes, in chromosome and gene mapping, in the generation  
CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for  
CC generating transgenic animals or knockout animals, to construct  
CC hybridisation probes for mapping the gene which encodes the PRO  
CC polypeptide, and for the genetic analysis of individuals with genetic  
CC disorders, in gene therapy, for chromosome identification, as  
CC chromosome markers, and for generating probes for PCR, Northern  
CC analysis, Southern analysis and Western analysis. The present  
CC sequence represents a human PRO cDNA clone.  
CC Note: The sequence data for this patent was obtained in electronic  
CC format directly from the USPTO web site at  
CC [seqdata.uspto.gov/psipsidentry.html](http://seqdata.uspto.gov/psipsidentry.html).  
CC  
SQ Sequence 466 BP; 116 A; 77 C; 115 G; 149 T; 9 other;  
  
Query Match 27.2%; Score 28; DB 25; Length 466;  
Best Local Similarity 59.7%; Pred No. 21;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
  
QY 5 TGACGTGATTAACAGTTTATGACAGCATTAATAGCTCCGATATGTAATGCTAATA 64  
DB 216 TGAGTGGTTTAAATCTTTCATGCTGGATTAATAACAGCTGCATCATATATCCACA 157  
QY 65 CAGCTTAAAAAACGGTA 81  
DB 156 CCGTGTAAAAAATAGTA 140  
  
RESULT 34  
ABX16976/C  
ID ABX16976 standard; cDNA; 466 BP.  
XX  
AC ABX16976;  
XX  
DT 04-FEB-2003 (first entry)  
XX  
DE Human PRO polynucleotide #163.  
XX  
XX Human; PRO; gene; ss; secreted polypeptide; transmembrane polypeptide;  
KW toxin; radiolabel; cell death; gene mapping; chromosome mapping;  
KW protein electrophoresis; genetic disorder; immunosuppressive; cytostatic;  
antibacterial.  
XX  
OS Homo sapiens.  
XX  
PN US2002123463-A1.  
XX  
PD 05-SEP-2002.  
XX  
PF 19-NOV-2001; 2001US-0989732.  
XX  
XX 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US21108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 16-DEC-1999; 99WO-US28634.  
PR 20-DEC-1999; 99WO-US30095.  
PR 06-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 03-JUN-1998; 98US-087759P.  
PR 04-JUN-1998; 98US-088021P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088326P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088743P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088858P.  
PR 11-JUN-1998; 98US-088861P.  
PR 12-JUN-1998; 98US-088876P.  
PR 16-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089532P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089598P.  
PR 17-JUN-1998; 98US-089599P.  
PR 17-JUN-1998; 98US-089600P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 28-AUG-2001; 2001US-0941992.



XX (GENENTECH INC.  
 PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
 XX Ferrera N, Fong S, Genter H, Gerritsen ME, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gurey AL, Kijaviri IU, Napier MA, Pan J, Paoi NF,  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
 PI Zhang Z;  
 DR WPI: 2003-066810/06.  
 XX  
 PT Novel secreted and transmembrane polypeptide for modulating biological  
 PT activity of cell expressing the polypeptide, identifying agonists or  
 PT antagonists of polypeptide, and as molecular weight markers  
 XX  
 PS Disclosure: Fig 60: 655pp; English.  
 XX  
 CC The invention relates to a secreted and transmembrane polypeptide, termed  
 CC PRO polypeptide, and the polynucleotide encoding it. The polypeptide is  
 CC useful for detecting PRO polypeptides and for linking a bioactive  
 CC molecule to a cell expressing the above polypeptides, where the bioactive  
 CC molecule is a toxin, radiolabel or an antibody. The bioactive material  
 CC causes the death of the cell. The polypeptide is useful for identifying  
 CC agonists or antagonists of the PRO polypeptide, for preparing variants of  
 CC PRO, as a molecular weight marker for protein electrophoresis purposes  
 CC and the PRO polynucleotide is useful for recombinantly expressing those  
 CC markers. The polynucleotide is also useful as a hybridisation probe, in  
 CC chromosome and gene mapping, in generation of antisense RNA and DNA, in  
 CC the preparation of PRO polypeptide, for generating transgenic animals or  
 CC knockout animals which in turn are useful in the development and  
 CC screening of therapeutically useful reagents, to construct hybridisation  
 CC probes for mapping the gene which encodes PRO and for the genetic  
 CC analysis of individuals with genetic disorders, in gene therapy, for  
 CC chromosome identification, as a chromosome marker and for generating  
 CC probes for PCR, Northern analysis, Southern analysis and Western  
 CC analysis. This sequence represents a human PRO polynucleotide of the  
 CC invention.  
 CC  
 SQ Sequence 466 BP; 116 A; 77 C; 115 G; 149 T; 9 other;  
 XX  
 Query Match 27.2%; Score 28; DB 25; Length 466;  
 Best Local Similarity: 59.7%; Pred. No. 21;  
 Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
 QY 5 TGACGAGATTAACAGTTAATGACACGATTAATAGCTCTGATATGTAATGCTAATA 64  
 DB 216 TGAAGTGTAAATCTTCAATGCTGATTAATACAGCTCATATGATTAATCCACCA 157  
 QY 65 CAGTTAAAAAAGCGTA 81  
 DB 156 CCTGTAAAAAATAGTA 140  
 XX  
 RESULT 35  
 ABS76828/c  
 ID ABS76828 standard; cDNA; 725 BP.  
 XX  
 AC ABS76828;  
 XX  
 DT 12-DEC-2002 (first entry)  
 XX  
 DE Frog embryonic gene sequence Q9925237 #1.  
 XX  
 KW Frog; ss; embryonic development; developmental disorder;  
 KW microarray; cell differentiation.  
 XX  
 OS Xenopus laevis.  
 XX  
 OS US2002081610-A1.  
 XX  
 PN 27-JUN-2002.  
 PD  
 PF 23-JUL-2001; 2001US-0910943.  
 XX  
 PF

XX 21-JUL-2000; 2000US-219658P.  
 PR  
 XX (UNIQ ) UNIV ROCKEFELLER.  
 PA  
 XX Hemmati-Briylanlou A, Altman CR;  
 PI WPI: 2002-626534/67.  
 DR  
 PT Nucleic acid array containing Xenopus embryonic nucleic acids is useful  
 PT to identify genes involved in embryonic development, to identify  
 PT different types of embryonic cells, and to diagnose developmental  
 PT disorders  
 XX  
 PS Claim 1; Page 98; 823pp; English.  
 XX  
 CC The invention relates to a nucleic acid array, where each coordinate  
 CC contains a single nucleic acid species having one of 770 nucleotide  
 CC sequences (appearing as ABS76747-ABS77516) a of a Xenopus embryonic gene  
 CC product, or its complement or hybridisable fragment of not less than  
 CC 20 contiguous nucleotides of one of those sequences. Also included are  
 CC detecting differential expression of embryonic genes, comprising:  
 CC (a) contacting a nucleic acid array comprising genes expressed in  
 CC embryonic but not mature cells with nucleic acids from sample and  
 CC control cells; and (b) detecting differential hybridisation of nucleic  
 CC acids from the sample cells relative to the control cells; and detecting  
 CC defects in development, comprising: (a) contacting nucleic acids from  
 CC test cells undergoing development with a nucleic acid array of gene  
 CC products known to play a fundamental role in the development process; and  
 CC (b) detecting a difference in expression of a fundamental gene in the  
 CC sample cells relative to a standard. The invention is useful to identify  
 CC genes involved in embryonic development and related processes such as  
 CC cell differentiation. This would be useful for diagnosing developmental  
 CC disorders and for identifying different types of embryonic cells.  
 CC The present sequence is one of the 770 Xenopus embryonic cDNA sequences.  
 CC  
 SQ Sequence 725 BP; 215 A; 137 C; 165 G; 206 T; 2 other;  
 XX  
 Query Match 27.2%; Score 28; DB 24; Length 725;  
 Best Local Similarity 58.3%; Pred. No. 23;  
 Matches 49; Conservative 0; Mismatches 35; Indels 0; Gaps 0;  
 QY 9 TGAATTAACAGTTAATGACAGCATTAATAGCTTCATATGTAATGCTAATACAGT 68  
 DB 664 TGTCAATTCCTTTTAACGCAATGTAATATCTTGTTCTGTGCTTTCGATTAACGT 605  
 QY 69 TAAAAAAGCGTATTTCCCTGTT 92  
 DB 604 TTGACCAATGATATGCTTCTT 581  
 XX  
 RESULT 36  
 ABS76832/c  
 ID ABS76832 standard; cDNA; 725 BP.  
 XX  
 AC ABS76832;  
 XX  
 DT 12-DEC-2002 (first entry)  
 XX  
 DE Frog embryonic gene sequence Q9925237 #2.  
 XX  
 KW Frog; ss; embryonic development; developmental disorder;  
 KW microarray; cell differentiation.  
 XX  
 OS Xenopus laevis.  
 XX  
 OS US2002081610-A1.  
 XX  
 PN 27-JUN-2002.  
 PD  
 PF 23-JUL-2001; 2001US-0910943.  
 XX  
 PF 21-JUL-2000; 2000US-219658P.  
 XX



Query Match	Best Local Similarity	Score	DB	Length
Matches 47; Conservative 2; Mismatches 34; Indels 0; Gaps 0;	27.0%;	27.8;	22;	378;
XX	AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)			
CC	amino acid sequences given in AAK62170 to AAK91921. (I) have cytosolic			
CC	activity, and can be used in gene therapy and vaccine production. (I)			
CC	proteins and polynucleotides may be used in the prevention, diagnosis and			
CC	treatment of diseases associated with inappropriate (I) expression. For			
CC	example, they may be used to treat disorders associated with decreased			
CC	expression by rectifying mutations or deletions in a patient's genome			
CC	that affect the activity of (I) by expressing inactive proteins or to			
CC	supplement the patients own production of (I). Additionally, (I)			
CC	polynucleotides may be used to produce the secreted (I), by inserting			
CC	the nucleic acids into a host cell and culturing the cell to express the			
CC	protein. (I) proteins and polynucleotides may be used to prevent,			
CC	diagnose and treat immune/hematopoietic-related diseases, especially			
CC	cancers and cancer metastases of haematopoietic-derived cells. AAK64703			
CC	to AAK67694 represent human immune/hematopoietic antigen genomic			
CC	sequences from the present invention. AAK54942 to AAK54950 and AAK62169			
CC	represent sequences used in the exemplification of the present invention.			
XX	Sequence 378 BP; 125 A; 60 C; 71 G; 117 T; 5 other:			
OY	19. GTTAAATGACAGCATTTAATAGCTCCTCGCATATGTGAAATGCTAAATACAGTTAAAAAAGC 78			
Db	9 GGTTCCTTAACAGATTAATTAATATACCCAGCTTAATTTTAAAGACTTTTAAATAT 68			
OY	79 GTATTTCCCTGGTTCTGATCCA 101			
Db	69 GTGTTTCATRTTAAGGAACAAA 91			
RESULT 38				
AAAC81718c				
ID	AAAC81718 standard; DNA; 2024 BP.			
XX	AAAC81718;			
AC				
XX	26-FEB-2001 (first entry)			
DT				
XX	Human secreted protein coding sequence SEQ ID NO: 19.			
DE				
XX	Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;			
KW	antiallergic; hepatoprotective; antididiabetic; antiinflammatory; antifur;			
KW	vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;			
KW	cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;			
KW	neurological disease; infection; human; secreted protein; ss.			
XX				
OS	Homo sapiens.			
XX				
XX	WO20061627-A1.			
PN				
XX	19-OCT-2000.			
PD				
XX	06-APR-2000; 2000WO-US09067.			
PF				
XX	09-APR-1999; 99US-0128697.			
PR				
XX	20-JAN-2000; 2000US-0176929.			
XX				
PA	(HUMA-) HUMAN GENOME SCI INC.			
XX	(ROSE/) ROSEN C A.			
PI	Rosen CA, Ruden SM, Komatsoulis G;			
XX				
XX	WPI: 2000-647419/62.			
DR				
XX	P-PSDB; AAB45394.			
PT	New nucleic acid molecules encoding 49 human secreted proteins for			
XX	diagnosing, preventing, treating or ameliorating medical conditions and			
XX	used as food additives or preservatives -			

XX	Example 2; Page 9; 10pp: Japanese.	
PS		
CC	The present sequence is alpha-1.3-multi-branch dextran hydrolase gene.	
CC	This sequence was derived from <i>Sphingobacterium</i> sp. V-54. This sequence	
CC	can be used for the recombinant preparation of alpha-1.3-multi-branch	
CC	dextran hydrolase.	
CC		
XX		
SQ	Sequence 2166 BP; 721 A; 390 C; 465 G; 590 T; 0 other;	
	Query Match	26.8%; Score 27.6; DB 22; Length 2166;
	Best Local Similarity	60.8%; Pred. No. 39;
	Matches	45; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
OY	28 CAGCATTTAATAGTCCTGCATATGTCATATGCTAATACAGTTAAATAACGATATTTCC	87
Db	2029 CAGCATTAATATGTTGCCAATAAGSTCACTTCCTTCATCCAGAAAAATCAATTTATCTTCG	1970
OY	88 TGGTTCTGCATCCAA 101	
Db	1969 ATGTTCTGCTGGAA 1956	
	RESULT 40	
	AA188906	
ID	AA188906 standard; cDNA; 2552 BP.	
XX		
AC	AA188906;	
XX		
DT	06-NOV-2001 (first entry)	
DE	Human polynucleotide SEQ ID NO 8966.	
XX		
XX	Human; cytokine; cell proliferation; cell differentiation; gene therapy;	
KM	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;	
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;	
KW	nervous system disorders; arthritis; inflammation; ss.	
XX		
OS	Homo sapiens.	
XX		
XX	WO200164835-A2.	
PN		
PD	07-SEP-2001.	
XX		
PE	26-FEB-2001; 2001WO-US04927.	
XX		
PR	28-FEB-2000; 2000US-0515126.	
PR	18-MAY-2000; 2000US-0577409.	
XX		
XX	(HYSE-) HYSEQ INC.	
PA		
XX		
PI	Tang YT, Liu C, Drmanac RT;	
XX		
XX	WPI; 2001-514838/56.	
DR	P-PSDB; AAO08975.	
XX		
PT	Isolated nucleic acids and polypeptides, useful for preventing	
PT	diagnosing and treating e.g. leukaemia, inflammation and immune	
XX	disorders -	
XX		
PS	Claim 1; SEQ ID NO 8966; 1399pp + Sequence Listing; English.	
XX		
CC	The invention relates to human polynucleotides (AA179941-AA193841) and	
CC	the encoded proteins (AA000010-AA013910) that exhibit activity elating to	
CC	cytokine, cell proliferation or cell differentiation or which may induce	
CC	production of other cytokines in other cell populations. The	
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or	
CC	peptide therapy. The polypeptides have various cytokine-like activities,	
CC	e.g. stem cell growth factor activity, haematopoiesis regulating	
CC	activity, tissue growth factor activity, immunomodulatory activity and	
CC	activity/inhbin activity and may be useful in the diagnosis and/or	
CC	treatment of cancer, leukaemia, nervous system disorders, arthritis and	
CC	inflammation.	

cc contaminated by other proteolytic enzymes. For expression of

Db 2256 ATAGAGAGCTTACTATATCATTTATTAAGTAGCATATATTACTTCAAAATACCTATATT 2315

OY 73 AAACGTAATTCCTGCTGTTCTGATCCAC 102  
DB 2316 AGAAGATATGATCTGACTGAATATTAAC 2345

## RESULT 43

ABV47128  
ID ABV47128 standard; cDNA; 444 BP.

AC ABV47128;

DT 16-SEP-2002 (first entry)

DE Human prostate expression marker cDNA 47119.

KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
pharmacogenomic marker; gene; ss.

OS Homo sapiens.

PN WO200160860-A2.

PD 23-AUG-2001.

PF 20-FEB-2001; 2001WO-US05171.

PR 17-FEB-2000; 2000US-183319P.

PR 16-MAR-2000; 2000US-189862P.

PR 25-MAY-2000; 2000US-207454P.

PR 09-JUN-2000; 2000US-211314P.

PR 18-JUL-2000; 2000US-219007P.

PR 13-DEC-2000; 2000US-255281P.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Endege WO, Monahan JE;

PT WPI; 2001-662795/76.

PS Claim 1; Page 9277; 11750pp; English.

CC The invention relates to an isolated nucleic acid molecule (I) comprising  
a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

CC specification or its complement. (I) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate  
cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;

CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
patient;

CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

CC Sequence 444 BP; 129 A; 107 C; 71 G; 137 T; 0 other;

OY 9 TGGATACAGTTTATATACAGATTATAGCTCTGATATGTAATGCTAATACAGT 68  
DB 151 TGAATATGCTATCCATGCTTACATGATTTATTTCAAAATTTTGGTAAATAGT 210  
OY 69 TAAAAAAGGATTTCCCTGTTCTGATCCA 101

DB 211 TTAGAAAACATTTATATTTTGTAAATATTTCCA 243

## RESULT 44

AB241332  
ID AB241332 standard; DNA; 588 BP.

AC AB241332;

DT 07-MAR-2003 (first entry)

DE N. gonorrhoeae nucleotide sequence SEQ ID 7253.

KW Antibacterial; infection; vaccine; gene therapy; gene; ds.

OS Neisseria gonorrhoeae.

PN WO200279243-A2.

PD 10-OCT-2002.

PF 12-FEB-2002; 2002WO-IB02069.

PR 12-FEB-2001; 2001GB-0003424.

PA (CHIR-) CHIRON SPA.

PI Fontana MR, Pizsa M, Masianni V, Monaci E;

PR WPI; 2003-058415/05.

PR P-PSDB; ABP80362.

PT New protein from Neisseria gonorrhoeae, useful for the manufacture of a  
medicament for treating or preventing N. gonorrhoeae infection

PS Disclosure; Page 715; 815pp; English.

CC The present invention relates to proteins from Neisseria gonorrhoeae.  
CC Also disclosed are the nucleic acid molecules encoding the proteins and  
CC antibodies that specifically bind to the proteins. The composition

CC comprising the protein, nucleic acid or antibody is useful for the  
CC manufacture of a medicament for treating or preventing N. gonorrhoeae  
CC infection, this may be in the form of a vaccine or gene therapy.

CC Sequences given in records AB237706-AB242016 represent nucleic acid  
CC molecules of the invention.

CC Sequence 588 BP; 186 A; 112 C; 122 G; 168 T; 0 other;

OY 25 TGACAGCAATTAATACCTCTGATATGTAATGCTAATACGTTAAAAACGATATT 84  
DB 287 TGTACAACTAAATAATTCCTGTAATGCTATTTAAATACGTAACCAACATTTT 346

OY 85 C 85

DB 347 C 347

Query Match 26.6%; Score 27.4; DB 25; Length 588;  
Best Local Similarity 65.6%; Pred. No. 35;  
Matches 40; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

OY 25 TGACAGCAATTAATACCTCTGATATGTAATGCTAATACGTTAAAAACGATATT 84  
DB 287 TGTACAACTAAATAATTCCTGTAATGCTATTTAAATACGTAACCAACATTTT 346

OY 85 C 85

DB 347 C 347

## RESULT 45

AB241770  
ID AB241770 standard; DNA; 588 BP.

AC AB241770;

DT 07-MAR-2003 (first entry)

DE N. gonorrhoeae nucleotide sequence SEQ ID 8129.

KW Antibacterial; infection; vaccine; gene therapy; gene; ds.

XX Neisseria gonorrhoeae.  
OS  
XX  
PN WO200279243-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 12-FEB-2002; 2002WO-1B02069.  
XX  
PR 12-FEB-2001; 2001GB-0003424.  
XX  
PA (CHIR-) CHIRON SPA.  
XX  
PI Fontana MR, Pizsa M, Maignani V, Monaci E;  
XX WPI; 2003-058415/05.  
DR P-PSDB; ABP80800.  
XX  
PT New protein from Neisseria gonorrhoeae, useful for the manufacture of a  
XX medicament for treating or preventing N. gonorrhoeae infection -  
XX  
PS Disclosure; Page 781; 815pp; English.  
XX  
CC The present invention relates to proteins from Neisseria gonorrhoeae.  
CC Also disclosed are the nucleic acid molecules encoding the proteins and  
CC antibodies that specifically bind to the proteins. The composition  
CC comprising the protein, nucleic acid or antibody is useful for the  
CC manufacture of a medicament for treating or preventing N. gonorrhoeae  
CC infection, this may be in the form of a vaccine or gene therapy.  
CC Sequences given in records AB237706-AB242016 represent nucleic acid  
XX molecules of the invention.  
XX  
SQ Sequence 588 BP; 186 A; 112 C; 122 G; 168 T; 0 other;  
XX  
Query Match 26.6%; Score 27.4; DB 25; Length 588;  
Best Local Similarity 65.6%; Pred. No. 35;  
Matches 40; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
QY 25 TGACAGCATTAATAGCTCCTGCATATGTAATGCTAATACAGTTAAAAACGGTATTT 84  
Db 287 TGTACAACTAAATAATCTCTGTAATGTGTATTTAAATAACGTAATAAACACCATTTT 346  
QY 85 C 85  
Db 347 C 347

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Job time : 181 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 25, 2003, 06:47:22 ; Search time 1595 Seconds

(without alignments)  
2641.813 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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1:  gb.ba:*
2:  gb.htg:*
3:  gb.in:*
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6:  gb.pat:*
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10: gb.ro:*
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22: em.ph:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55.2	53.6	12793	6 AX119931	AX119931 Sequence
2	55.2	53.6	12793	9 AF193556	AF193556 Homo sapi
3	55.2	53.6	92693	9 AL157766	AL157766 Human DNA
4	55.2	53.6	99819	2 AC079761	AC079761 Homo sapi
5	53.6	52.0	11492	6 AX119933	AX119933 Sequence
6	53.6	52.0	11493	10 AF193557	AF193557 Mus muscu
7	53.6	52.0	283096	2 AC138718	AC138718 Mus muscu
8	49	47.6	722	11 BV018667	BV018667 S21P6240
9	48.8	47.4	240277	2 AC126559	AC126559 Rattus no
10	37.6	36.5	92309	2 AC021908	AC021908 Homo sapi
11	36.2	35.1	74962	6 AR253940	AR253940 Sequence
12	36.2	35.1	74962	6 AX350371	AX350371 Sequence
13	36.2	35.1	190648	6 CWS01DX1	AL139317 Human chr
14	34.4	33.4	291738	2 AC097744	AC097744 Mus muscu
15	33.8	32.8	156547	10 AC117262	AC117262 Mus muscu
16	33.8	32.8	177843	10 AL928639	AL928639 Mouse DNA
17	33.8	32.8	248044	2 BX284649	BX284649 Mus muscu
18	33.2	32.2	172022	2 AC134425	AC134425 Mus muscu
19	33.2	32.2	180219	9 AC099520	AC099520 Homo sapi
20	33.2	32.2	205222	2 AC130698	AC130698 Mus muscu
21	32.8	31.8	554	11 BV000942	BV000942 S209P6376
22	32.8	31.8	40033	9 HS1110P6	AL049175 Human DNA
23	32.6	31.7	156493	2 AC141553	AC141553 Rattus no
24	32.6	31.7	209701	2 AC111966	AC111966 Rattus no
25	32.6	31.7	252839	2 AC095096	AC095096 Rattus no
26	32.6	31.7	256498	2 AC118378	AC118378 Rattus no
27	32.6	31.7	263259	2 AC121737	AC121737 Rattus no
28	32.4	31.5	159598	2 AP004386	AP004386 Homo sapi
29	32.4	31.5	167153	2 AL954648	AL954648 Danio rer
30	32.4	31.5	197877	2 AC090142	AC090142 Homo sapi
31	32.4	31.5	198176	2 AC069127	AC069127 Homo sapi
32	32.4	31.5	205394	2 AL954337	AL954337 Danio rer
33	32.4	31.5	207756	2 AC021546	AC021546 Homo sapi
34	32.4	31.1	57810	2 AC125433	AC125433 Homo sapi
35	32	31.1	95616	9 AC104655	AC104655 Homo sapi
36	32	31.1	132120	9 AC026733	AC026733 Homo sapi
37	32	31.1	137331	2 AC015774	AC015774 Homo sapi
38	32	31.1	172387	2 AC103561	AC103561 Homo sapi
39	32	31.1	191682	2 AC062005	AC062005 Homo sapi
40	31.8	30.9	214165	2 BX469936	BX469936 Danio rer
41	31.8	30.9	248948	2 AC097421	AC097421 Rattus no
42	31.6	30.7	1604	6 AX702602	AX702602 Sequence
43	31.6	30.7	110000	2 AC112392.1	AC112392.1 of
44	31.6	30.7	110000	2 AC112392.2	AC112392.2 of
45	31.6	30.7	110000	2 AC124223.0	AC124223 Rattus no

#### ALIGNMENTS

```

RESULT 1
AX119931
LOCUS AX119931 12793 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 1 from Patent WO0129266.
ACCESSION AX119931
VERSION AX119931.1 GI:14036678
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Hudson,T.J., Engert,J. and Richter,A.
AUTHORS Identification of arsacs mutations and methods of use therefor
TITLE Patent: WO 0129266-A 1 26-APR-2001;
JOURNAL

```

FEATURES  
source  
McGILL UNIVERSITY (CA) : Hopital Sainte-Justine (CA)  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
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BASE COUNT  
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ORIGIN

Query Match  
Best Local Similarity 75.0%; Pred. No. 2.4e-05;  
Matches 69; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GAAGTACGTAATTAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTAATTGCT 60  
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DB 6543 GAAGTACGTAATTAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTAATTGCT 6602  
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QY 61 AATACAGTTAAAAAAGCGTATTTCCTGCTT 92  
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DB 6603 TAATACAGTTAAAAAAGCGTATTTCCTGCTT 6634

RESULT 2  
AF193556 12793 bp DNA linear PRI 07-FEB-2000  
LOCUS  
DEFINITION  
AF193556 Homo sapiens saccin (SACS) gene, complete cds.  
ACCESSION  
AF193556.1 GI:6907041  
VERSION  
AF193556.1  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 12793)  
Engert,J.C., Berube,P., Mercier,J., Dore,C., Lepage,P., Ge,B.,  
Bouchard,J.P., Mathieu,J., Melancon,S.B., Schalling,M.,  
Lander,E.S., Morgan,K., Hudson,T.J. and Richter,A.  
ARSCS, a spastic ataxia common in northeastern Quebec, is caused  
by mutations in a new gene encoding an 11.5-kb ORF  
Nat. Genet. 24 (2), 120-125 (2000)  
20120709  
10655055  
2 (bases 1 to 12793)  
Engert,J.C., Berube,P., Dore,C., Lepage,P., Ge,B., Hudson,T.J. and  
Richter,A.  
Direct Submission  
Submitted (08-OCT-1999) Genome Centre, Montreal General Hospital,  
1650 Cedar Ave., Montreal, QC H3G 1A4, Canada  
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ETPKVCGGALCSLQGRQLQLLSBOFTGLIRIKKHENDNAFLANERKARILCNAFLR  
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KYSFOEFTYSNMCEATSHKSEROONKKEKPSAQOTYQRFVFPYFKSVGNPEVAR  
RMLROARANEFSARNDLKRNANEMVCFYCYSTKTLALIAADYAVGKSDKVPALPA  
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ACITIKLENFMOKY"

BASE COUNT  
4163 a 2256 c 2487 g 3887 t

ORIGIN

Query Match  
Best Local Similarity 75.0%; Pred. No. 2.4e-05;  
Matches 69; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GAAGTACGTAATTAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTAATTGCT 60  
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DB 6543 GAAGTACGTAATTAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTAATTGCT 6602  
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QY 61 AATACAGTTAAAAAAGCGTATTTCCTGCTT 92  
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Db 6603 TAATACAGTTAAAAACGATTTCCCTGCT 6634

RESULT 3  
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LOCUS  
DEFINITION Human DNA sequence from clone RP11-40020 on chromosome 11q12.11-12.2, complete sequence.  
ACCESSION AL157766  
VERSION AL157766  
KEYWORDS GI:13620292  
SOURCE HTG.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eulhelia; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE Tromans, A.  
AUTHORS Tromans, A.  
TITLE Direct Submission  
JOURNAL Submitted (11-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CE10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
COMMENT  
Requests: clonerequest@sanger.ac.uk  
On Apr 12, 2001 this sequence version replaced gi:12709868.  
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; SW, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at  
http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chr13  
RP11-40020 is from the library RPCT-11.1 constructed by the group of Pieter de Jong. For further details see  
http://www.chori.org/Dacpac/home.htm  
VECTOR: pBACE3.6  
IMPORTANT: This sequence is not the entire insert of clone RP11-40020. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.  
The true left end of clone RP11-760M1 is at 92594 in this sequence. The true right end of clone RP11-72P19 is at 100 in this sequence.  
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2562..2673  
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3896..4201  
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5122..5397  
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repeat\_region  
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20613..20912  
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repeat_region 71780. .72075
/note="Alusk repeat: matches 1. .295 of consensus"
repeat_region 72145. .72256
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Query Match 53.6%; Score 55.2; DB 9; Length 92693;
Best Local Similarity 75.0%; Pred. No. 1.9e-05;
Matches 69; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
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DEFINITION
AC079761.1 GI:10047966
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Center: Washington University Genome Sequencing Center
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information
NOTE: This is a 'working draft' sequence. It currently
consists of 44 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
1
1138 1137: contig of 1137 bp in length
1238 1237: gap of unknown length
1238 2538: contig of 1301 bp in length
2539 2638: gap of unknown length
2639 3977 3976: contig of 1338 bp in length
3977 4076: gap of unknown length
4077 5355: contig of 1279 bp in length
5356 5455: gap of unknown length
5456 6757: contig of 1302 bp in length
6758 6857: gap of unknown length
6858 8570: contig of 1713 bp in length
8571 8670: gap of unknown length
8671 9925: contig of 1255 bp in length
9926 10025: gap of unknown length
10026 11426: contig of 1401 bp in length
11427 11526: gap of unknown length
11527 13266: contig of 1740 bp in length
13267 13366: gap of unknown length
13367 14794: contig of 1428 bp in length
14795 14894: gap of unknown length
14895 16054: contig of 1160 bp in length
16055 16154: gap of unknown length
16155 17395: contig of 1241 bp in length
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19388 21294: contig of 1907 bp in length
21295 21394: gap of unknown length
21395 22944: contig of 1550 bp in length
22945 23044: gap of unknown length
23045 24421: contig of 1377 bp in length
24422 24521: gap of unknown length
24522 25870: contig of 1349 bp in length
25871 27230: gap of unknown length
27231 27330: contig of 1260 bp in length
27331 gap of unknown length
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* 28779 28878: gap of unknown length
* 30879 30893: contig of 2015 bp in length
* 30894 30993: gap of unknown length
* 32460 32460: contig of 1467 bp in length
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* 32561 33984: contig of 1424 bp in length
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* 34085 35285: contig of 1201 bp in length
* 35286 35385: gap of unknown length
* 35386 37184: contig of 1799 bp in length
* 37185 37284: gap of unknown length
* 37285 39172: contig of 1888 bp in length
* 39173 39272: gap of unknown length
* 39273 40874: contig of 1602 bp in length
* 40875 40974: gap of unknown length
* 40975 42893: contig of 1919 bp in length
* 42894 42993: gap of unknown length
* 42994 44384: contig of 1391 bp in length
* 44385 44484: gap of unknown length
* 44485 45999: contig of 1515 bp in length
* 46000 46099: gap of unknown length
* 46100 48669: contig of 2570 bp in length
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* 52810 52909: gap of unknown length
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* 55128 55227: gap of unknown length
* 55228 58087: contig of 2860 bp in length
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* 58188 61004: contig of 2817 bp in length
* 61005 61104: gap of unknown length
* 61105 64185: contig of 3081 bp in length
* 64186 64285: gap of unknown length
* 64286 67105: contig of 2820 bp in length
* 67106 67205: gap of unknown length
* 67206 70837: contig of 3632 bp in length
* 70838 70937: gap of unknown length
* 70938 75937: contig of 4900 bp in length
* 75938 75937: gap of unknown length
* 75938 80452: contig of 4515 bp in length
* 80453 80552: gap of unknown length
* 80553 84661: contig of 4109 bp in length
* 84662 84761: gap of unknown length
* 84762 90542: contig of 5781 bp in length
* 90543 90642: gap of unknown length
* 90643 94348: contig of 3706 bp in length
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* 94449 99819: contig of 5371 bp in length.

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Best Local Similarity 75.0%; Pred. No. 1.9e-05;
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QY 1 GAACTGACTGGAATTAACAGTTTAATGACAGCATTAATAGCTCTGCATATGTGAATTGCT 60
DB 86952 GAACTGACTGGAATTAACAGTTTAATGACAGCATTAATAGCTCTGCATATGTGAATTGCT 86893

QY 61 AATACAGTTAATAAAGCGTATTTCCTCGGTT 92
DB 86892 TAAATACAGTTAATAAAGCGTATTTCCTCGGTT 86861

RESULT 5
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LOCUS	AX119933	11492 bp	DNA	Linear	PAT 11-MAY-2001
DEFINITION	Sequence 3 from Patent W00129266.				
ACCESSION	AX119933				
VERSION	AX119933.1	GI:14036679			
KEYWORDS					
SOURCE					
ORGANISM	Mus musculus (house mouse)				
REFERENCE					
AUTHORS	1 Hudson, T.J., Engert, J. and Richter, A.				
TITLE	Identification of arasac mutations and methods of use therefor				
JOURNAL	Patent: WO 0129266-A 3 26-Apr-2001;				
	McGILL UNIVERSITY (CA) ; Hopital Sainte-Justine (CA)				
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OY	61 AATTCAGTTAAAAAACGCTATTTCCCTGCT 92				
Db	6526 TAATCAGTTAAAAAACGCTATTTCCCTGCT 6557				
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DEFINITION	Mus musculus sacs1n gene, complete cds.				
ACCESSION	AF193557				
VERSION	AF193557.1	GI:6907043			
KEYWORDS					
SOURCE					
ORGANISM	Mus musculus (house mouse)				
	Mus musculus				
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 11493)				
AUTHORS	Engert, J.C., Berube, P., Mercier, J., Dore, C., Lepage, P., Ge, B.,				
	Bouchard, J.P., Mathieu, J., Melancon, S.B., Schalling, M.,				
	Lander, E.S., Morgan, K., Hudson, T.J. and Richter, A.				
	ASACS, a spastic ataxia common in northeastern Quebec, is caused				
	by mutations in a new gene encoding an 11.5-kD ORF				
	Nat. Genet. 24 (2), 120-125 (2000)				
JOURNAL	20120709				
MEDLINE	10655055				
PUBMED	2 (bases 1 to 11493)				
REFERENCE	Engert, J.C., Berube, P., Dore, C., Lepage, P., Ge, B., Hudson, T.J. and				
AUTHORS	Richter, A.				
TITLE	Direct Submission				
JOURNAL	Submitted (08-OCT-1999) Genome Centre, Montreal General Hospital,				
	1650 Cedar Ave., Montreal, QC H3G 1A4, Canada				
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CDS	1. 11493				
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OY	61	AATACAGTTAAAAAACGGTATTTCGCCGGTT	92		
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LOCUS	AC138718	283096 bp	DNA	linear	HTG 25-FEB-2003
DEFINITION	Mus musculus chromosome UKM clone RP23-221F8, WORKING DRAFT				
ACCESSION	AC138718				
VERSION	AC138718.1	GI:27753855			
KEYWORDS	HTG; HTGS; PHASE1; HTGS_DRAFT; HTGS_FULLTOP.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 283096)				
AUTHORS	McPherson,J.D. and Waterston,R.H.				
TITLE	The sequence of Mus musculus clone				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 283096)				
AUTHORS	McPherson,J.D. and Waterston,R.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (15-JAN-2003) Genome Sequencing Center, 4444 Forest Park				
REFERENCE	Parkway, St. Louis, MO 63108, USA				
AUTHORS	3 (bases 1 to 283096)				
TITLE	McPherson,J.D. and Waterston,R.H.				
JOURNAL	Direct Submission				
REFERENCE	Submitted (25-FEB-2003) Genome Sequencing Center, 4444 Forest Park				
AUTHORS	Parkway, St. Louis, MO 63108, USA				
COMMENT					
	----- Genome Center -----				
	Center: Washington University Genome Sequencing Center				
	Center code: WUGSC				
	Web site: http://genome.wustl.edu/gsc/index.shtml				
	Contact: submissions@wustl.wustl.edu				
	----- Project Information -----				
	Center project name: M_BA0221F08				
	----- Summary Statistics -----				
	Sequencing vector: M13; 0%				
	Sequencing vector: plasmid; 100%				
	Chemistry: Dye-primed ET; 0% of reads				
	Chemistry: Dye-terminator Big Dye; 100% of reads				
	Assembly program: Phrap; version 0.990319				
	Consensus quality: 282412 bases at least Q40				
	Consensus quality: 283029 bases at least Q30				
	Consensus quality: 283429 bases at least Q20				
	Insert size: 218000; agarose-IP				
	Insert size: 286547; sum-of-contigs				
	Quality coverage: 18.55 in Q20 bases; agarose-IP				
	Quality coverage: 12.13 in Q20 bases; sum-of-contigs				
	----- NOTE: This is a 'working draft' sequence. It currently				
	* consists of 4 contigs. The true order of the pieces				
	* is not known and their order in this sequence record is				
	* arbitrary. Gaps between the contigs are represented as				
	* runs of N, but the exact sizes of the gaps are unknown.				
	* This record will be updated with the finished sequence				
	* as soon as it is available and the accession number will				
	* be preserved.				
	1				
	33704: contig of 33704 bp in length				
	33705	33804: gap of unknown length			
	33805	85933: contig of 52129 bp in length			
	85934	86033: gap of unknown length			
	86034	154253: contig of 66220 bp in length			

FEATURES	* 154354	154353:	gap of unknown length
source	* 154354	283096:	contig of 128743 bp in length.
		Location/Qualifiers	
	1..283096	/organism="Mus musculus"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:10090"	
		/chromosome="XNK"	
		/clone="RP23-221F8"	
misc_feature	1..33704	/note="assembly_name:Contig50"	
	33805..85933		
misc_feature	/note="assembly_name:Contig51"		
	86034..1154253		
misc_feature	/note="assembly_name:Contig52"		
	154354..283096		
	/note="assembly_name:Contig53"		
BASE COUNT	79658 a	61811 c	61785 g 79513 t 329 others
ORIGIN			
Query Match	52.0%;	Score 53.6;	DB 2; Length 283096;
Best Local Similarity	73.9%;	Pred. No. 4.7e-05;	
Matches	68; Conservative	0; Mismatches 24; Indels	0; Gaps 0;
OY	1	GAAGTGCATGGATTAACAGTTTAAGACAGACGTTAATAGCTCCTGCATATGCAATTGCT	60
Db	249129	GAGGAGCATGGATTAATAGTTTAAGACAGCATTAAATACACCTGCATATGTTGAGTTAC	249070
OY	61	AATACAGTTAAAAACGTTATTTCCCTGGTT	92
Db	249069	TAAATCAGTTAAAAAACGTTATTTCCCTGGT	249038
RESULT 8			
LOCUS	BV018667	722 bp	DNA linear STS 30-MAY-2003
DEFINITION	S212P6240FH4.T0 CZECHII/El Mus musculus STS genomic sequence		
ACCESSION	BV018667		
VERSION	BV018667.1	GI:31102562	
KEYWORDS	STS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
	1 (bases 1 to 722)		
REFERENCE	Wade,C.M., Kulbokas,E.J. II, Kirby,A.W., Zody,M.C., Mullikin,J.C.,		
AUTHORS	Lander,E.S., Linblad-Toh,K. and Daly,M.J.		
	The mosaic structure of variation in the laboratory mouse genome		
TITLE	Nature 420 (6915), 574-578 (2002)		
JOURNAL	22354684		
MEDLINE	12466852		
PUBMED			
COMMENT			
	Contact: Kerstin Lindblad-Toh		
	Whitehead Institute for Biomedical Research, Center for Genome		
	Research		
	320 Charles Street, Cambridge, MA 02141, USA		
	Tel: 6172521477		
	Fax: 6172580903		
	Email: kerslin@genome.wi.mit.edu		
	Primer A: None		
	Primer B: None		
	STS size: 722		
	Protocol:		
	MGS-discovery: Paired-end low-coverage whole genome shotgun reads		
	were generated from 12951/SVIM, C3H/HeJ and BALB/cByJ. The MGS		
	reads were placed uniquely on the MGSv3 C57BL/6J assembly and SNP		
	detection was carried out by SSAHA-SNP. 225,000 reads were		
	annotated		
	as STS and 81,000 SNPs were annotated with alleles from C57BL/6J		
	and the strain from which the particular read came. The validation		
	rate for these SNPs was estimated at approximately 98%.		
	Location/Qualifiers		

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source
1. 722
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CzechII/E1"
/db_xref="taxon:10090"
/map="14 22-662 52304811-52305451"
/clone_11b="CzechII/E1"
<1..>722

STS
BASE COUNT 226 a 145 c 153 g 198 t
ORIGIN

Query Match
Best Local Similarity 91.2% Pred. No. 0.0018; Length 722;
Matches 52: Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAGTACTGCAATACAGTTTAAATGACAGCATTAATAGCTGCGATATGTAAT 57
653 GAAGTACTGCAATACAGTTTAAATGACAGCATTAATAGCTGCGATATGTTAGT 709

RESULT 9
AC126559
LOCUS
DEFINITION
AC126559 240277 bp DNA linear HTG 09-MAY-2003
Rattus norvegicus clone CH230-4E7, *** SEQUENCING IN PROGRESS ***
2 unordered pieces.
AC126559.5 GI:30466790
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
KEYWORDS
Rattus norvegicus (Norway rat)
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 240277)
Muzny,D,Marie, Metzger,M, Lee, Abramson,S, Adams,C, Alder,J,
Allen,C, Allen,H, Alsbrooks,S, Amin,A, Angiano,D,
Anyalbechi,V, Aoyagi,A, Ayodeji,M, Baca,E, Baden,H,
Baldwin,D, Bandaranaike,D, Barber,M, Barnstead,M, Benahmed,F,
Biswal,K, Blair,J, Blankenburg,K, Blyth,P, Brown,M,
Bryant,N, Buhay,C, Burch,P, Burrell,K, Calderon,E,
Cardenas,V, Carter,K, Cavazos,I, Ceasar,H, Center,A,
Chacko,J, Chavez,D, Chen,G, Chen,R, Chen,Y, Chen,Z, Chu,J,
Cleveland,C, Cockrell,R, Cox,C, Coyle,M, Cree,A, D'Souza,L,
Devila,M,L, Davis,C, Davy-Carroll,L, De Anda,C, Dederich,D,
Delgado,O, Denson,S, Deramo,C, Ding,Y, Dinh,H, Divya,K,
Drepper,H, Dugan-Rocha,S, Dunn,A, Durbin,K, Duval,B, Eaves,K,
Egan,A, Escotto,M, Eugene,C, Evans,C,A, Falls,T, Fan,G,
Fernandez,S, Finley,M, Flagg,N, Forbes,L, Foster,M, Foster,P,
Fraser,C,M, Gabisi,A, Ganta,R, Garcia,A, Garner,T, Garza,M,
Geregeorgis,E, Geer,K, Gill,R, Grady,M, Guerra,W, Guevara,W,
Gunnarsson,P, Haaland,W, Hamill,C, Hamilton,C, Hamilton,K,
Harvey,Y, Havlak,P, Hawes,A, Henderson,N, Hernandez,R,
Hernandez,R, Hines,S, Hladun,S,L, Hodgson,A, Hogues,M,
Hollins,B, Howells,S, Hulik,S, Hummel,J, Idlebird,D, Jackson,A,
Jackson,L, Jacob,L, Jiang,H, Johnson,B, Johnson,R, Jolivet,A,
Karpathy,S, Kelly,S, Kelly,S, Khan,Z, King,L, Kovar,C,
Kowis,C, Kraft,C,L, Lebow,H, Levan,J, Lewis,L, Li,Z, Liu,J,
Liu,J, Liu,W, Liu,Y, London,P, Longacre,S, Lopez,J,
Lorensunhewa,L, Louisedge,H, Lozada,R,J, Lu,X, Ma,J,
Maheshwari,M, Mahindartne,M, Mahmoud,M, Malloy,K, Mangum,A,
Mangum,B, Mapue,P, Martin,K, Martin,R, Martinez,E,
Mahoney,S, McLeod,M,P, McNeill,T,Z, Meenen,E,
Miosavljivic,A, Miner,G, Minja,E, Montemayor,J, Moore,S,
Morgan,M, Morris,K, Morris,S, Munidasa,M, Murphy,M, Nair,L,
Nankervis,C, Neal,D, Newton,N, Nguyen,N, Norris,S,
Nwaokemelehu,C, Okuwonu,G, Olarunpasegun,A, Pal,S, Parks,K,
Pasternak,S, Paul,H, Perez,A, Perez,L, Plannoch,C,
Plopper,F, Polidexter,A, Popovic,D, Primus,E, Pu,L,L,
Puzo,M, Quiroz,J, Rachlin,E, Reeves,K, Regier,M,A, Reigh,R,
Rellly,B, Rellly,M, Ren,Y, Reuter,M, Richards,S, Riggs,F,
Rives,C, Rodkey,T, Rojas,A, Rose,M, Rose,R, Ruiz,S,J,
Sanders,W, Savery,G, Scherer,S, Scott,G, Shatsman,S, Shen,H,
Shetty,J, Shvartsbeyn,A, Sisson,I, Sitter,C,D, Smaj,D,

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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steinle,M., Strong,R., Sutton,A., Sytek,A., Taber,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tinney,A., Trejos,Z., Umanli,K.,
Vais,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Wilson,R., Wlczynk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,I., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 240277)
Worley,K.C.
Direct Submission
Submitted (07-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 240277)
Rat Genome Sequencing Consortium.
Submitted (09-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 9, 2003 this sequence version replaced gi:25188888.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GATV
Center clone name: CH230-4E7
----- Summary Statistics
Assembly program: Atlas
Consensus quality: 228324 bases at least Q40
Consensus quality: 230189 bases at least Q30
Consensus quality: 231614 bases at least Q20
Estimated insert size: 240669; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 239107: contig of 239107 bp in length
* 239108 239207: gap of unknown length
* 239208 240277: contig of 1070 bp in length.
Location/Qualifiers
1. 240277
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-4E7"
complement(237792..238683)
FEATURES
source
misc_feature

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/note="clone_boundary
clone_end:Sp6
site:EcORI
end_sequence:BH305315"
BASE COUNT 62798 a 52456 c 51438 g 66166 t 7419 others
ORIGIN

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Query Match	47.4%	Score 48.8	DB 2	Length 240277
Best Local Similarity	70.7%	Pred. No. 0.001		
Matches 65	Conservative 0	Mismatches 27	Indels 0	Gaps 0

Oy 1GAAGTACGACGGATTAACAGTTTAAATGACACGCATTATAGCTCCCTCATATGTGAATTGCT 60  
| | | | |  
Db 125163 GCAGTGACTGGACAATAGTTTAAATGACAGCCTTATAAGCGCCCTGCATATGTTGCAATTAC 125222

```

QY      61 AATACAGTTAAAAAACGGTATTTCCCTGGTT  92
          | | | | | | | | | | | | | |
Db      125223 TAATCCAGTTAAAAAACGGTATTTCCCTGGT 125256

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RESULT 10  
AC021908  
.....

ACCESSION	AC021908
VERSION	AC021908.2
	GI:9123999

ORGANISM      Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi

AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E  
 TITLE Homo sapiens, clone RP11-21G21

**AUTHORS**  
2 (cases 1 & 2) 2507  
Biren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,  
Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,

Canevaro, I., Colanagelo, M., Collins, S., Collumple, A., Cooke, F., DeArellano, K., Dewar, K., Donno, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,

Landers, T., Lehoczky, J., Levine, R., Liu, C., Liu, G., Locke, K., MacDonald, P., Marquis, N., McEwan, P., McGuir, A., McKernan, K., Newman, D., Robinson, R., Jones, C., Kamm, E., Katsikas, A., Kitchin, J.,

Mohman, C. R., O Connell, L., O Donnell, P., Oliva, J. M., Peterson, K.,  
Pierre, N., Plisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,  
Roy, A., Santos, R., Severy, P., Spencer, B., Strange-Thomann, N.

TITLE  
Direct Submission  
Zimmer, A. and Zody, M.  
Iltis, A., Vassiliou, H., Vial, R., Vo, A., Wu, X.,  
Wyman, D., Ye, W. U

COMMENT  
research, 320 Chaires Street, Cambridge, MA 02141, USA  
On Jul 13, 2000 this sequence version replaced gi:6730876.  
All repeats were identified using RepeatMasker.

Center: Whitehead Institute/ MIT Center for Genome Research  
-----  
Genome Center  
-----  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

```

Web site: http://www-seq.wi.mit.edu
Contact: sequence\_submissions@genome.wi.mit.edu
----- Protect Information -----

```

```

-----
Center clone name: 21_G_21
-----
* NOTE: This record contains 01 individual(s)

```

- \* contigs. Runs of N are used to separate the reads
- \* and the order in which they appear is completely

- \* arbitrary low-pass sequence sampling is useful for
- \* identifying clones that may be gene-rich and allows
- \* overlap relationships among clones to be deduced.
- \* However, it should not be assumed that this clone
- \* will be sequenced to completion. In the event that
- \* the record is updated, the accession number will
- \* be preserved.

*	1	914: contig of 914 bp in length
*	915	1014: gap of 100 bp
*	1015	1937: contig of 923 bp in length
*	1938	2037: gap of 100 bp

*	2038	2974:	contig of 937 bp in length
*	2975	3074:	gap of 100 bp
*	3075	3993:	contig of 919 bp in length
*	3994	4093:	gap of 100 bp

*	4094	4988: contig of 895 bp in length
*	4989	5088: gap of 100 bp
*	5089	6006: contig of 918 bp in length
*	6007	6106: gap of 100 bp

*	6107	7012: contig of 906 bp in length
*	7013	7112: gap of 100 bp
*	7113	8033: contig of 921 bp in length
*	8034	8133: gap of 100 bp

```

*      8134      9051: contig of 918 bp in length
*      9052      9151: gap of 100 bp
*      9152      10086: contig of 935 bp in length
*      10087      10186: gap of 100 bp

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*	10187	11089:	contig of 903 bp in length
*	11090	11189:	gap of 100 bp
*	11190	12084:	contig of 895 bp in length
*	12085	12184:	gap of 100 bp

*	14111	ran of 100 bp
*	14210	ran of 100 bp
*	13218	contig of 893 bp
*	13118	gap of 100 bp
*	13117	contig of 933 bp
*	12185	contig of 933 bp
*	12185	contig of 933 bp

14211	gap of 100 bp
14212	conf of 910 bp in length
15121	gap of 100 bp
15220	gap of 100 bp
16155	conf of 935 bp in length
16255	gap of 100 bp
16156	gap of 100 bp

16256	gap of 100 bp
16257	contig of 932 bp in length
17188	gap of 100 bp
17287	gap of 100 bp
18206	contig of 919 bp in length
18208	gap of 100 bp

18267	gap of 100 bp
18307	contig of 934 bp in length
19241	gap of 100 bp
19340	gap of 100 bp
20262	contig of 922 bp in length
20263	gap of 100 bp

	gap of 100 bp	contig of 905 bp	gap of 100 bp	contig of 905 bp	gap of 100 bp	contig of 905 bp	gap of 100 bp	contig of 905 bp
20362	gap of 100 bp		21267	contig of 905 bp	21267	contig of 905 bp	21267	contig of 905 bp
20363	gap of 100 bp		21267	contig of 905 bp	21267	contig of 905 bp	21267	contig of 905 bp
21268	gap of 100 bp		21267	contig of 905 bp	21267	contig of 905 bp	21267	contig of 905 bp
21368	gap of 100 bp		21267	contig of 905 bp	21267	contig of 905 bp	21267	contig of 905 bp
22271	gap of 100 bp		21267	contig of 905 bp	21267	contig of 905 bp	21267	contig of 905 bp
22271	gap of 100 bp		21267	contig of 905 bp	21267	contig of 905 bp	21267	contig of 905 bp

*	2227/2	gap of 100 bp
*	2237/1	gap of 909 bp in length
*	23280	contig of 100 bp
*	23380	gap of 100 bp
*	23381	contig of 920 bp in length
*	24300	contig of 100 bp
*	24301	contig of 100 bp

	24301	24400	24401	25318	25319	25419	26340
*	gap of 100 bp						
*		contig of 918 bp					
*			gap of 100 bp				
*				contig of 922 bp			

*	26341	26440: gap of 100 bp
*	26441	27333: contig of 893 bp in length
*	27334	27433: gap of 100 bp
*	27434	28339: contig of 906 bp in length

	28340	28439	gap of 100 bp
*	28440	29335	contig of 896 bp in length
*	29336	29435	gap of 100 bp
*	29436	30361	contig of 926 bp in length

*	30362	30461: gap of 100 bp
*	30462	31348: contig of 887 bp in length
*	31349	31448: gap of 100 bp
*	31449	32386: contig of 938 bp in length

*	32387	32486: gap of 100 bp
*	32487	33411: contig of 925 bp in length
*	33412	33511: gap of 100 bp

33512 34425: contig of 914 bp in length  
34426 34525: gap of 100 bp  
34526 35410: contig of 885 bp in length  
35410 35510: gap of 100 bp  
35510 35511: gap of 100 bp  
35511 36426: contig of 916 bp in length  
36426 36526: gap of 100 bp  
36526 37433: contig of 907 bp in length  
37433 37533: gap of 100 bp  
37533 38477: contig of 944 bp in length  
38477 38577: gap of 100 bp  
38577 39478: contig of 901 bp in length  
39478 39578: gap of 100 bp  
39578 40485: contig of 907 bp in length  
40485 40585: gap of 100 bp  
40585 41532: contig of 947 bp in length  
41532 41632: gap of 100 bp  
41632 42546: contig of 914 bp in length  
42546 43567: gap of 100 bp  
43567 43667: contig of 921 bp in length  
43667 43668: gap of 100 bp  
43668 44591: contig of 924 bp in length  
44591 44592: gap of 100 bp  
44592 44591: contig of 900 bp in length  
44591 45591: gap of 100 bp  
45591 46615: contig of 924 bp in length  
46615 46715: gap of 100 bp  
46715 47612: contig of 897 bp in length  
47612 47713: gap of 100 bp  
47713 48632: contig of 920 bp in length  
48632 48732: gap of 100 bp  
48732 49654: contig of 922 bp in length  
49654 49754: gap of 100 bp  
49754 50648: contig of 894 bp in length  
50648 50749: gap of 100 bp  
50749 51644: contig of 896 bp in length  
51644 51745: gap of 100 bp  
51745 52675: contig of 931 bp in length  
52675 52775: gap of 100 bp  
52775 53719: contig of 944 bp in length  
53719 53820: gap of 100 bp  
53820 54715: contig of 896 bp in length  
54715 54815: gap of 100 bp  
54815 55729: contig of 914 bp in length  
55729 55829: gap of 100 bp  
55829 56761: contig of 932 bp in length  
56761 56861: gap of 100 bp  
56861 57754: contig of 893 bp in length  
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57854 58754: contig of 900 bp in length  
58754 58854: gap of 100 bp  
58854 59778: contig of 924 bp in length  
59778 59878: gap of 100 bp  
59878 60804: contig of 926 bp in length  
60804 60904: gap of 100 bp  
60904 61841: contig of 937 bp in length  
61841 61941: gap of 100 bp  
61941 62870: contig of 929 bp in length  
62870 62971: gap of 100 bp  
62971 63885: contig of 915 bp in length  
63885 63985: gap of 100 bp  
63985 64902: contig of 917 bp in length  
64902 65002: gap of 100 bp  
65002 65914: contig of 912 bp in length  
65914 66918: gap of 100 bp  
66918 67018: contig of 904 bp in length  
67018 67931: gap of 100 bp  
67931 68031: contig of 913 bp in length  
68031 68901: gap of 100 bp  
68901 69001: contig of 870 bp in length  
69001 69902: contig of 901 bp in length  
69902 70002: gap of 100 bp  
70002 70936: contig of 934 bp in length

Query Match  
Best Local Similarity 36.5%; Score 37.6; DB 2; Length 92309;  
Matches 55; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 18 AGTTTATGACACATTATAGCTCGCATATGTGTAATGCTAATACAGTTAAACAAAC 77  
Db 91089 AGTGTATATAGTACATGAAATGCTGTCTTAAGTGTATGATGCAAAATACATTAAAGAAAC 91148  
Qy 78 GGATTTCCCTGGTCTGATCAAA 101  
Db 91149 AGTATTCCTGGTCAATATCAAA 91172

RESULT 11  
AR253940/c AR253940 74962 bp DNA linear PAT 20-DEC-2002  
LOCUS Sequence 3 from patent US 6479270.  
DEFINITION AR253940  
ACCESSION AR253940  
VERSION AR253940.1 GI:27302425  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 74962)  
AUTHORS Wei,M.-H., Ketchum,K.A., Di Francesco,V. and Beasley,E.M.  
TITLE Isolated human phosphatase proteins, nucleic acid molecules  
encoding human phosphatase proteins, and uses thereof  
JOURNAL Patent: US 6479270-A 3 12-NOV-2002;  
FEATURES  
source 1. 74962  
BASE COUNT 21639 a 14055 c 14307 g 24824 t 137 others

Query Match  
Best Local Similarity 35.1%; Score 36.2; DB 6; Length 74962;  
Matches 56; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 12 AATACAGTTTATGACACATTATAGCTCGCATATGTGTAATGCTAATACAGTTAA 71  
Db 63338 AAAAAAAAAAATTCACATCAAGACCTAGAGACTTACTTTCAATCAATTA 63279  
Qy 72 AAAACGTAATTCCTGGTCTGATCCA 100  
Db 63278 AAAAAGCTTTCAGTACTTCACACTA 63250

RESULT 12  
AX350371/c AX350371 74962 bp DNA linear PAT 06-FEB-2002  
LOCUS Sequence 3 from Patent WO0160992.  
DEFINITION AX350371  
ACCESSION AX350371  
VERSION AX350371.1 GI:18616029  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1 Wei,M.-H., Ketchum,K.A., di Francesco,V.C. and Beasley,E.M.  
AUTHORS Human protein tyrosine phosphatase; encoding dna and uses thereof  
TITLE Patent: WO 0160992-A 3 23-AUG-2001;  
JOURNAL PE Corporation (NY) (US)  
FEATURES  
source 1. 74962  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 21639 a 14055 c 14307 g 24824 t 137 others

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ORIGIN
Query Match      35.1%; Score 36.2; DB 6; Length 74962;
Best Local Similarity 62.9%; Pred. No. 3.6;
Matches 56; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

OY      12 AATAACGTTTAAGACGATTAATGCTTCATATGATGCTATATACAGTTAA 71
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      63338 AAAAAAAAAAATTCACGATTCAGAACCTTAGACACTTACTTTCTATCAATTAA 63279
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY      72 AAAAAAGGTATTTCCCTGCTTCATCCA 100
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      63278 AAAAAAGGTCTTTCAGTACTTCATCTA 63250
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
CNS01DXI/LOCUS 190648 bp DNA linear PRI 04-MAY-2001
DEFINITION Human chromosome 14 DNA sequence BAC R-589M4 of library RPCT-11
ACCESSION AL139317
VERSION AL139317.5 GI:13992185
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 190648)
AUTHORS Heilig,R., Petit,J.L., Vilco,V., Dasilva,C., Robert,C., Winkler,P.,
            Brolier,P., Catolico,L., Barbe,V., Pelleier,E., Artiguenave,F.,
            Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Crnaud,C.,
            Gyapay,G., Saurin,W. and Weissenbach,J.
            Sequencing of the human chromosome 14
            Unpublished
            2 (bases 1 to 190648)
            Genoscope.
            Direct Submission
            Submitted (04-MAY-2001) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)
            - Web : www.genoscope.cns.fr)
            On May 8, 2001 this sequence version replaced g1:11611152.
            ----- Genom Center
            Center: genoscope / Centre National de Sequencage
            Center code: GS
            Web site: http://www.genoscope.cns.fr/
            Contact: Sequef@genoscope.cns.fr
            -----
            The following BAC sequence is oriented from the T7 to the SP6 end.
            ----- Summary Statistics
            Assembly program: Phrap: version 2.0
            Quality coverage: 9.67x in Q20 bases; sum-of-contigs
            -----
            Overall quality chart :
            Range : bases
            0 :
            1 - 9 :
            10 - 19 :
            20 - 29 : 6
            30 - 39 :
            40 - 49 : 50
            50 - 59 : 1311
            60 - 69 : 4326
            70 - 79 : 16979
            80 - 89 : 49761
            90 - 99 : 111972
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            Percentage of bases with a quality value >= 40 : 99 %.
FEATURES
SOURCE
            Location/Qualifiers
            1..190648
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

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/chrosome="14"
/clone="R-589M4"
/clone_lib="RPCT-11"
33101..33202
/note="matching EMBL:G30493
RHdb:RH95349
RHdb:RH37979
dbSTS:STS32646
Identified using the e-PCR software (G. Schuler)"
33210..33333
/note="matching EMBL:H89509
RHdb:RH44742
dbSTS:STS37810
Identified using the e-PCR software (G. Schuler)"
33302..33483
/note="matching EMBL:AA875827
RHdb:RH93777
dbSTS:STS66770
Identified using the e-PCR software (G. Schuler)"
35098..35185
/note="matching EMBL:R12383
RHdb:RH99190
dbSTS:STS68938
Identified using the e-PCR software (G. Schuler)"
115234..115355
/note="matching EMBL:D59713
RHdb:RH47352
dbSTS:STS40412
Identified using the e-PCR software (G. Schuler)"
116229..116369
/note="matching EMBL:H29253
RHdb:RH44425
RHdb:RH15723
dbSTS:STS20542
Identified using the e-PCR software (G. Schuler)"

BASE COUNT      58113 a 37509 c 37884 g 57142 t

ORIGIN
Query Match      35.1%; Score 36.2; DB 9; Length 190648;
Best Local Similarity 62.9%; Pred. No. 3.3;
Matches 56; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

OY      12 AATAACGTTTAAGACGATTAATGCTTCGATGTAATGCTATATACAGTTAA 71
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      32488 AAAAAAAAAAATTCACGATTCAGAACCTTAGACACTTACTTTCTATCAATTAA 32429
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY      72 AAAAAAGGTATTTCCCTGCTTCATCCA 100
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Db      32428 AAAAAAGGTCTTTCAGTACTTCATCTA 32400
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
AC097744      291738 bp DNA linear HTG 10-MAY-2003
LOCUS AC097744
DEFINITION Rattus norvegicus clone CH230-11M4, WORKING DRAFT SEQUENCE, 2
unordereed pieces.
ACCESSION AC097744
VERSION AC097744.9 GI:30521774
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULFILLP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
            1 (bases 1 to 291738)
            Muzny,D., Marie, Mettler,M., Lee, Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Albrooks,S., Amin,A., Angiano,D.,
            Anyalebechi,V., Ayogaji,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,

```



JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 156547)  
 AUTHORS McPherson, J.D. and Waterston, R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (08-APR-2002) Genome Sequencing Center, 4444 Forest Park  
 Parkway, St. Louis, MO 63108, USA  
 REFERENCE 3 (bases 1 to 156547)  
 AUTHORS McPherson, J.D. and Waterston, R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-MAY-2002) Genome Sequencing Center, 4444 Forest Park  
 Parkway, St. Louis, MO 63108, USA  
 REFERENCE 4 (bases 1 to 156547)  
 AUTHORS McPherson, J.D. and Waterston, R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-JUN-2002) Genome Sequencing Center, 4444 Forest Park  
 Parkway, St. Louis, MO 63108, USA  
 COMMENT On May 16, 2002 this sequence version replaced gi:20069850.

----- Genome Center -----  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: <http://genome.wustl.edu/gsc/index.shtml>  
 Contact: [submissions@watson.wustl.edu](mailto:submissions@watson.wustl.edu)  
 Project Information  
 Center project name: M\_BB0537M07

FEATURES  
 source  
 1. 156547  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 /clone="RP24-537M7"

BASE COUNT 47059 a 32654 c 31502 g 45332 t  
 ORIGIN  
 Query Match 32.8%; Score 33.8; DB 10; Length 156547;  
 Best Local Similarity 58.4%; Pred. No. 15;  
 Matches 59; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
 QY 1 GAAGTACGTGGAATACAGTTTAATGACAGCATTAATGCTCCGTCATATGTAATGCT 60  
 DB 139738 GTATTGGCTTTAGACATATATTCATTATTCATTGTTAACTATGATCAAGTAATTTGGG 139797  
 QY 61 AATACAGTTAAAAAAGCGTATTCCCGTTCGATCCAA 101  
 DB 139798 AGTATTTCTATAAATGATATTAGAGGTTCTGAGTCAA 139838

RESULT 16  
 AL928639/c 177843 bp DNA linear ROD 31-OCT-2002  
 LOCUS Mouse DNA sequence from clone RP23-446017 on chromosome 2, complete  
 DEFINITION sequence.  
 ACCESSION AL928639  
 VERSION AL928639.5 GI:24474486  
 KEYWORDS HTG.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 177843)  
 Bates, K.  
 Direct Submission  
 Submitted (31-OCT-2002) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
[humquerry@sanger.ac.uk](mailto:humquerry@sanger.ac.uk) Clone requests: [clonerequest@sanger.ac.uk](mailto:clonerequest@sanger.ac.uk)  
 On Nov 1, 2002 this sequence version replaced gi:24414771.  
 COMMENT ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: <http://www.sanger.ac.uk>  
 Contact: [humquerry@sanger.ac.uk](mailto:humquerry@sanger.ac.uk)

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats: all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPEP; Information on the WormPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) RP23-446017 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACe3.6.

FEATURES  
 source  
 1. 177843  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 /chromosome="2"  
 /clone="RP23-446017"  
 /clone\_11b="RPCI-23"

BASE COUNT 52840 a 36061 c 35495 g 53447 t  
 ORIGIN  
 Query Match 32.8%; Score 33.8; DB 10; Length 177843;  
 Best Local Similarity 58.4%; Pred. No. 15;  
 Matches 59; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
 QY 1 GAAGTACGTGGAATACAGTTTAATGACAGCATTAATGCTCCGTCATATGTAATGCT 60  
 DB 127561 GTATTGGCTTTAGACATATATTCATTATTCATTGTTAACTATGATCAAGTAATTTGGG 127502  
 QY 61 AATACAGTTAAAAAAGCGTATTCCCGTTCGATCCAA 101  
 DB 127501 AGTATTTCTATAAATGATATTAGAGGTTCTGAGTCAA 127461

RESULT 17  
 BX284649/c 248044 bp DNA linear HTG 08-MAY-2003  
 LOCUS Mus musculus chromosome 2 clone RP23-42M7, \*\*\* SEQUENCING IN  
 DEFINITION PROGRESS \*\*\*, 3 unordered pieces.  
 ACCESSION BX284649  
 VERSION BX284649.11 GI:30519649  
 KEYWORDS HTG; HTGS; PHASE1; HTGS\_ACTIVIFIN; HTGS\_DRAFT; HTGS\_FULLTOP.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 248044)  
 Johnson, C.  
 Direct Submission  
 Submitted (07-MAY-2003) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
[humquerry@sanger.ac.uk](mailto:humquerry@sanger.ac.uk) Clone requests: [clonerequest@sanger.ac.uk](mailto:clonerequest@sanger.ac.uk)  
 On May 10, 2003 this sequence version replaced gi:30550058.  
 COMMENT ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: <http://www.sanger.ac.uk>

Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 Mus musculus, clone RP24-26655  
 Unpublished  
 2 (bases 1 to 172022)  
 Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,  
 Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B.,  
 Camarata,J., Chang,J., Chazaro,B., Choquel,Y., Collymore,A.,  
 Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,  
 Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,  
 Gardyna,S., Gird,S., Graham,L., Grand-Pierre,N., Hagos,B.,  
 Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kanat,A.,  
 Karas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,  
 Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,  
 McCarthy,M., Meldrim,J., Menus,L., Mihova,T., Mienga,V.,  
 Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,  
 O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,  
 Phunhhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,  
 Roman,J., Roy,A., Schauer,S., Schupbach,R., Seaman,S., Severy,P.,  
 Smith,C., Spence,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,  
 Tefaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,  
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,  
 Zemke,L., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (26-SEP-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 172022)  
 Birren,B., Nusbaum,C., Lander,E., Aboueleil,A., Allen,N.,  
 Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,  
 Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Choquel,Y.,  
 Collymore,A., Cook,A., Cooke,P., Corum,B., Dearellano,K.,  
 Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,  
 Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,  
 Graham,L., Grand-Pierre,N., Hatz,N., Hagopian,D., Hagos,B.,  
 Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,  
 Kanat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,  
 Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., Maclean,C.,  
 Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,  
 Meldrim,J., Menus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J.,  
 Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,  
 O'Neill,D., Oliver,J., Peterson,K., Phunhhang,P., Pierre,N.,  
 Rachpaka,A., Ramasamy,J., Raymond,C., Retta,R., Rise,C., Rogov,P.,  
 Roman,J., Schauer,S., Schupbach,R., Seaman,S., Severy,P.,  
 Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,  
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 Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,  
 Wyman,D., Young,G., Zainoun,J., Zemke,L., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (12-MAR-2003) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Mar 12, 2003 this sequence version replaced gi:28275012.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RN/RepeatMasker.html  
 -----  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WtBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 -----  
 Project Information  
 Center project name: L27143  
 Center clone name: 266\_E-5  
 -----  
 Summary Statistics  
 Sequencing vector: Plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 170825 bases at least Q40  
 Consensus quality: 171283 bases at least Q30  
 Consensus quality: 171504 bases at least Q20  
 Insert size: 174000; agarose-fp  
 Insert size: 171622; sum-of-ctrls  
 Quality coverage: 9.2 in Q20 bases; agarose-fp  
 Quality coverage: 9.4 in Q20 bases; sum-of-ctrls  
 -----  
 \* NOTE: This is a 'working draft' sequence. It currently







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Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,  
Henderson, D., Hines, C., Hudson, S., Hudson, A., Hughes, M.

Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,  
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Kowis, C., Kraft, C., Ledow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,  
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,  
Lorenshew, L., Louised, H., Lozano, R. J., Lu, X., Ma, J.,  
Maheshwari, M., Mahindarane, M., Mahmoud, M., Malloy, K., Mangum, A.,  
Mawney, S., McLeod, M., McNeill, T., Meenen, E., Milosavljevic, A.,  
Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K.,  
Morris, S., Mundasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D.,  
Newton, N., Nguyen, N., Norris, S., Nwackelme, O., Okunnu, G.,  
Olanunsgoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H.,  
Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A.,  
Popovic, D., Primus, E., Pu, L., L., Puazo, M., Quito, R., Rachlin, E.,  
Reeves, K., Regier, M., A., Reigh, R., Kelly, B., Kelly, M., Ken, Y.,  
Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A.,  
Rose, M., Rose, R., Ruiz, S. J., Sanders, M., Savery, G., Scherer, S.,  
Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A.,  
Sisson, I., Slater, C. D., Smajs, D., Sneed, A., Sodergren, E.,  
Song, X., Z., Sorrelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A.,  
Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S.,  
Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseana, D.,  
Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J.,  
Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlaczek, R.,  
Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S.,  
Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, D., Zhou, J., Zhou, X.,  
Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D. R.,  
Holt, R. A., Smith, H. O., Weinstein, G. and Gibbs, R. A.

Unpublished  
2 (bases 1 to 156493)  
Worley, K. C.

Direct Submission  
Submitted (17-MAR-2003) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information  
Center project name: KRBX  
Center clone name: CH230-123N13  
----- Summary Statistics  
Sequencing vector: Plasmid  
Chemistry: Dye-terminator Big Dye 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 130692 bases at least Q40  
Consensus quality: 139963 bases at least Q40  
Consensus quality: 147828 bases at least Q20  
Estimated insert size: 135973; sum-of-coverage estimation  
Quality coverage: 2x in Q20 bases; sum-of-coverage estimation

-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_drafc\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_drafc_data.html)).  
\* NOTE: This is a "working draft" sequence. It currently  
\* consists of 71 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1  
1857: contig of 1857 bp in length  
1858  
1957: gap of unknown length  
1958  
3564: contig of 1607 bp in length  
3565  
3664: gap of unknown length  
3665  
5132: contig of 1468 bp in length  
5133  
5232: gap of unknown length  
5233  
6236: contig of 1004 bp in length  
6237  
6336: gap of unknown length  
6337  
7825: contig of 1489 bp in length

7826  
7926  
9500: contig of 1575 bp in length  
9501  
9601  
10817: contig of 1217 bp in length  
10818  
10917: gap of unknown length  
10918  
12217: contig of 1300 bp in length  
12218  
12317: gap of unknown length  
12318  
13580: contig of 1263 bp in length  
13581  
13680: gap of unknown length  
13681  
15147: contig of 1467 bp in length  
15148  
15247: gap of unknown length  
15248  
15607: contig of 1360 bp in length  
15608  
16707: gap of unknown length  
16708  
18076: contig of 1369 bp in length  
18077  
18176: gap of unknown length  
18177  
19193: contig of 1017 bp in length  
19194  
19293: gap of unknown length  
20517: contig of 1224 bp in length  
20518  
20617: gap of unknown length  
22094: contig of 1477 bp in length  
22095  
22195: gap of unknown length  
22196  
23313: contig of 1119 bp in length  
23314  
23413: gap of unknown length  
24834: contig of 1421 bp in length  
24835  
24935: gap of unknown length  
24936  
26737: contig of 1803 bp in length  
26738  
27952: gap of unknown length  
27953  
28052: gap of unknown length  
28053  
29433: contig of 1361 bp in length  
29434  
29533: gap of unknown length  
29534  
30847: contig of 1314 bp in length  
30947: gap of unknown length  
32471: contig of 1524 bp in length  
32571: gap of unknown length  
32572  
34474: contig of 1903 bp in length  
34475  
34575: gap of unknown length  
36825: contig of 2251 bp in length  
36826  
36925: gap of unknown length  
38141: contig of 1216 bp in length  
38241: gap of unknown length  
38242  
39344: contig of 1103 bp in length  
39345  
39444: gap of unknown length  
41224: contig of 1780 bp in length  
41225  
41324: gap of unknown length  
42495: contig of 1171 bp in length  
42496  
42595: gap of unknown length  
43688: contig of 1093 bp in length  
43689  
43788: gap of unknown length  
46190: contig of 2302 bp in length  
46191  
46190: gap of unknown length  
48101: contig of 1911 bp in length  
48102  
48201: gap of unknown length  
50073: contig of 1872 bp in length  
50074  
50173: gap of unknown length  
51801: contig of 1628 bp in length  
51802  
51901: gap of unknown length  
53447: contig of 1546 bp in length  
53448  
53547: gap of unknown length  
54893: contig of 1346 bp in length  
54894  
54993: gap of unknown length  
56695: contig of 1702 bp in length  
56696  
56795: gap of unknown length  
58615: contig of 1820 bp in length  
58616  
58715: gap of unknown length  
60729: contig of 2014 bp in length  
60730  
60829: gap of unknown length  
63324: contig of 2495 bp in length  
63325  
63424: gap of unknown length  
64814: contig of 1390 bp in length  
64815  
64914: gap of unknown length  
66140: contig of 1226 bp in length  
66141  
66240: gap of unknown length

```

* 66241 68033: contig of 1793 bp in length
* 68034 68133: gap of unknown length
* 68134 69964: contig of 1831 bp in length
* 69964 70064: gap of unknown length
* 70064 72696: contig of 2632 bp in length
* 72696 72797: gap of unknown length
* 72797 74406: contig of 1610 bp in length
* 74406 74507: gap of unknown length
* 74507 76505: contig of 1999 bp in length
* 76505 76605: gap of unknown length
* 76605 79210: contig of 2604 bp in length
* 79210 81692: contig of 2383 bp in length
* 81692 81793: gap of unknown length
* 81793 83286: contig of 1494 bp in length
* 83286 83387: gap of unknown length
* 83387 85430: gap of 2044 bp in length
* 85430 85531: gap of unknown length
* 85531 87612: contig of 2082 bp in length
* 87612 87713: gap of unknown length
* 87713 90311: contig of 2599 bp in length
* 90311 90411: gap of unknown length

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Query Match 31.7% Score 32.6; DB 2: Length 156493;  
 Best Local Similarity 66.2%; Pred. No. 33;  
 Matches 47; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY 14 TAACAGTTTAAACAGCATTAAAGCTCCTGCATATGTAATGCTTAACAGTTAAAA 73  
 Db 102012 TAACAGTTTAAACAGCATTAAAGCTCCTGCATATGTAATGCTTAACAGTTAAAA 102071

OY 74 AACGCGATTT 84  
 Db 102072 AACGCGATTT 102082

RESULT 24  
 AC11966/c  
 LOCUS  
 DEFINITION  
 \*\*\*  
 AC11966 209701 bp DNA linear HTG 20-NOV-2002  
 Rattus norvegicus clone CH230-18504, \*\*\* SEQUENCING IN PROGRESS  
 \*\*\*  
 AC11966 GI:25139313  
 HTG: HTGS\_PHASE2: HTGS\_DRAFT: HTGS\_ENRICHED.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Rattus norvegicus (Norway rat)  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 209701)  
 Muzny, D., Marie, Metzker, M., Lee, Abramson, S., Adams, C., Alder, J.,  
 Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguliano, D.,  
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 Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,  
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 Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,  
 Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,  
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Li, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,  
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 Mangum, B., Mapua, P., Martin, R., Martin, R., Martinez, E.,  
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 Niederhausen, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,  
 Weinstock, G., and Gibbs, R. A.

WEINSTOCK, G. and GIBBS, R. A.  
 Direct Submission  
 Unpublished  
 2 (bases 1 to 209701)  
 Morley, K. C.  
 Direct Submission  
 Submitted (19-FEB-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 209701)  
 Rat Genome Sequencing Consortium.  
 Direct Submission  
 Submitted (20-NOV-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Nov 20, 2002 this sequence version replaced g1:23266189.  
 The sequence in this assembly is a combination of BAC based reads  
 and whole genome shotgun sequencing reads assembled using Atlas  
 (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described  
 in the feature table below represents a scaffold in the Atlas  
 assembly (a 'contig-scaffold'). Within each contig-scaffold,  
 individual sequence contigs are ordered and oriented, and separated  
 by sized gaps filled with Ns to the estimated size. The sequence  
 may extend beyond the ends of the clone and there may be sequence  
 contigs within a contig-scaffold that consist entirely of whole  
 genome shotgun sequence reads. Both end sequences and whole genome  
 shotgun sequence only contigs will be indicated in the feature  
 table.

----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: http://www.hgsc.bcm.tmc.edu/  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: GOYE  
 Center clone name: CH230-18504  
 ----- Summary Statistics  
 Assembly program: Phrap, version 0.990329  
 Consensus quality: 186401 bases at least Q40  
 Consensus quality: 189924 bases at least Q30  
 Consensus quality: 192483 bases at least Q20  
 Estimated insert size: 189616; sum-of-contigs estimation  
 Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

----- NOTE: Estimated insert size may differ from sequence length  
 (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 1 contigs. Gaps between the contigs

\* are represented as runs of N. The order of the pieces  
 \* is believed to be correct as given, however the sizes  
 \* of the gaps between them are based on estimates that have  
 \* provided by the submittor.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.

1 209701: contig of 209701 bp in length.  
 Location/Qualifiers

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/organism="Rattus norvegicus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10116"

/clone="CH230-18504"

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/note="wgs\_end-extension"

clone\_end:sp6"

3332..4135

/note="clone\_boundary"

clone\_end:sp6

site:

end\_sequence:BH266571"

101254..102704

/note="wgs\_contig"

102916..103994

/note="wgs\_contig"

complement(208485..209277)

/note="clone\_boundary"

clone\_end:t7

site:

end\_sequence:BH266569"

56455 a 42541 c 42380 g 52735 t 15590 others

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 31.7% Score 32.6; DB 2; Length 209701;

Matches 47; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 14 TAACAGTTTAAAGACGATTAATAGCTCGCATATGTGAATTCCTAATACAGTTAA 73

DB 105822 TAACAGTTTATTTGATTAATTAACCTCTTTATTTCTGAATGCTCTAATGTTCC 105763

QY 74 AACGCTATTT 84

DB 105762 AACGCTATTT 105752

RESULT 25

AC095096/c

LOCUS

DEFINITION

AC095096

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 252839)  
 Muzny, D., Marle, Metzger, M., Lee, Abramson, S., Adams, C., Alder, J.,  
 Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,  
 Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,  
 Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,  
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 Bryant, N., Buhay, C., Burch, P., Butrell, K., Calderon, E.,  
 Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A.,  
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 Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,  
 Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,  
 Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Diya, K.,  
 Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,

# COMMENT

## JOURNAL

## AUTHORS

## REFERENCE

## TITLE

## JOURNAL

## AUTHORS

## REFERENCE

## TITLE

## JOURNAL

## AUTHORS

## REFERENCE

## TITLE

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## JOURNAL

## AUTHORS

## REFERENCE

## TITLE

Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,  
 Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,  
 Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,  
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 Wierden, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,  
 Weinstock, G. and Gibbs, R. A.

# Unpublished

## 2 (bases 1 to 252839)

### Worley, K. C.

#### Direct Submission

##### Submitted (16-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

###### 3 (bases 1 to 252839)

###### Rat Genome Sequencing Consortium.

###### Direct Submission

###### Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 9, 2003 this sequence version replaced g1:24818178.  
 The sequence in this assembly is a combination of BAC based reads  
 and whole genome shotgun sequencing reads assembled using Atlas  
 (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described  
 in the feature table below represents a scaffold in the Atlas  
 assembly (a 'contig-scaffold'). Within each contig-scaffold,  
 individual sequence contigs are ordered and oriented, and separated  
 by sized gaps filled with Ns to the estimated size. The sequence  
 may extend beyond the ends of the clone and there may be sequence  
 contigs within a contig-scaffold that consist entirely of whole  
 genome shotgun sequence reads. Both end sequences and whole genome  
 shotgun sequence only contigs will be indicated in the feature  
 table.

# Genome Center

## Center: Baylor College of Medicine

### Center code: BCM

#### Web site: http://www.hgsc.bcm.tmc.edu/

##### Contact: hgsc-help@bcm.tmc.edu

###### Project Information

###### Center project name: GC1H

###### Center clone name: CH230-7G9

###### Summary Statistics

Assembly program: Atlas;  
Consensus quality: 248637 bases at least Q40  
Consensus quality: 249895 bases at least Q30  
Consensus quality: 250757 bases at least Q20  
Estimated insert size: 261226; sum-of-contigs estimation  
Quality coverage: 10x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_drift\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_drift_data.html))  
\* NOTE: This sequence may represent more than one clone.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 3 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

FEATURES	Location/Qualifiers
1	07000

```

/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-7G9"
1..1528

```

BASE COUNT	/note="wgs_config"			
ORIGIN	72063 a	54152 c	55812 g	69248 t
				1564 others

Query Match	31.7%;	Score 32.6;	DB 2;	Length 252839;
Best Local Similarity	60.9%;	Pred. No. 31;		
Matches 53; Conservative	0;	Mismatches 34;	Indels 0;	Gaps 0;

Qy	15	AAAGAGTTAATGACAGCATTAAATAGCTCCGCAATGTGTAATTCGTAATCAGTTAAAA	74
Db	201373	AAACGTTTGCACATTTTTCGCAAAAGCTCTTGTGTTAATGCATTAATAAATGCAATTATAA	2013144

QY 75 AACGGTATTTCCCTGGTTCGTATCCA 101  
+ + ||||| + + + +  
Db 201313 ATCTGATTTC CATGTCTATTCCTA 201287

RESULT 26  
AC118378

LOCUS	AC118378	256498 bp	DNA	linear	HTG 11-OCT-2002
DEFINITION	Rattus norvegicus clone CH230-35816,	***	SEQUENCING	IN PROGRESS	
REMARKS	*** 2 unordered pieces.				
ACCESSION	AC118378				

```

ACCESSION      AC118378.4
VERSION        GI:23618102
KEYWORDS       HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
SOURCE         Rattus norvegicus (Norway rat)
ORGANISM       Rattus norvegicus

```

REFERENCE  
AUTHORS  
1 (bases 1 to 256498)  
Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J. .,

Allen, C., Allen, H., Alsprocks, S., Amin, A., Angiano, D.,  
Anylebsch, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,  
Baldwin, D., Bandermanik, D., Barber, M., Bartscheid, M., Benahmed, F.,  
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,  
Byrant, N., Buhay, C., Burch, P., Butrell, K., Calderon, E.,  
Cardenas, V., Carter, K., Cavazos, I., Cesari, H., Centet, A.,  
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,  
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D Souza, L.,  
Davalila, M. L., Davis, C., Davy-Carrroll, L., De Anda, C., Dedertlich, D.,  
Delgado, O., Benson, S., Dermato, C., Ding, Y., Dinh, H., Divya, K.,  
Draper, H., Dugan-Rocha, S., Dunn, A., Durfin, K., Duval, B., Eaves, K.,

JOURNAL TITLE	Direct Submission
REFERENCE	2 (bases 1 to 256498)
AUTHORS	Worley, K.C.
JOURNAL TITLE	Direct Submission
JOURNAL TITLE	Submitted (17-APR-2002)
JOURNAL TITLE	Human Genome Sequencing Center, Department

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

3 (bases 1 to 256498)  
Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (11-OCT-2002) Human Genome Sequencing Center, Department

**COMMENT**

On Oct 9, 2002 this sequence version replaced g1:11746207. The sequence in this assembly is a combination of BAC-based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/atl/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

```

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Center project name: GRV
Center clone name: CH230-35816

----- Summary Statistics

```

Assembly program: Phrap, version 0.990329  
 Consensus quality: 183400 bases at least Q40  
 Consensus quality: 186096 bases at least Q30  
 Consensus quality: 187794 bases at least Q20  
 Estimated insert size: 190483; sum-of-contigs estimation  
 Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length  
 (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
 NOTE: This is a 'working draft' sequence. It currently  
 consists of 2 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.

1 255030: contig of 255030 bp in length  
 \* 255031 255130: gap of unknown length  
 \* 255131 256498: contig of 1368 bp in length.

## FEATURES

## SOURCE

Location/Qualifiers  
 1..256498

misc\_feature  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10116"  
 /clone="CH230-35816"  
 1..1782

misc\_feature  
 /note="wgs\_end\_extension  
 clone\_end:T"  
 2648..3813

misc\_feature  
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misc\_feature  
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 clone\_end:T"  
 7744..8660

misc\_feature  
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 site:MDOI

misc\_feature  
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 65259..66767  
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 192091..193784

misc\_feature  
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 complement(252911..253807)  
 /note="clone\_boundary  
 clone\_end:Sp6  
 site:MDOI

BASE COUNT 48109 a 43661 c 43433 g 54154 t 67141 others  
 ORIGIN

Query Match 31.7%; Score 32.6; DB 2; Length 256498;  
 Best Local Similarity 60.9%; Pred. No. 31;

Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

OY 15 AACGTTTATGACATTAATAGCTCTGCATATGTAATGCTAATACAGTTAAAA 74

Db 225021 AACGTTTACTATTTGTCACAAAGGCTCTGTTAATGATGAATAATTAATAA 225080

OY 75 AACGTTATTTCCCGGTTCTGATCCAA 101

Db 225081 ATCTGATTTTCCCATGTCCTAATTCCTA 225107

## RESULT 27

## AC121737/c

LOCUS 263259 bp DNA linear HTG 20-NOV-2002

DEFINITION Rattus norvegicus clone CH230-74A9, \*\*\* SEQUENCING IN PROGRESS \*\*\*;

## AC121737

AC121737 4 GI:25138094

KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ENRICHED.

## SOURCE

## ORGANISM

Rattus norvegicus (Norway rat)  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Rodentia; Sciurognathi; Muridae; Murinae;

## REFERENCE

## AUTHORS

1 (bases 1 to 263259)

Muzny,D.,Marie., Metzker,M.,Lee., Abramson,S., Adams,C., Alder,J.,  
 Allen,C., Allen,H., Alspbrooks,S., Amlin,A., Anguiano,D.,  
 Anyalebech,V., Ayagi,A., Ayodeji,M., Baca,E., Baden,H.,  
 Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benham,F.,  
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 Cardenas,V., Carter,K., Cavazos,I., Cesar,H., Center,A.,  
 Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,  
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 Davila,M.L., Davis,C., Davy-Carroll,L., De Ande,C., Dederich,D.,  
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 Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hognes,M.,  
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 Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C.,  
 Plapper,F., Polidexter,A., Popovic,D., Prims,E., Pu,L.,  
 Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Reiter,M.A., Relgh,R.,  
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 Rivers,C., Rodkey,T., Rojas,A., Rose,R., Rutz,S.J.,  
 Sanders,W., Savery,G., Scherer,S., Scott,G., Shatman,S., Shen,H.,  
 Shetty,J., Shvartsbeyn,A., Slison,I., Sitter,C.D., Smajls,D.,  
 Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,  
 Steimle,M., Strong,R., Sutton,A., Svetek,A., Taber,P., Taylor,C.,  
 Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,  
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 Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,  
 Williams,G., Willson,R., Wleczek,R., Wooden,H., Worley,K.,  
 Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,  
 Yu,F., Zhang,J., Zhou,J., Zhou,S., Zhao,S., Dunn,D., von  
 Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,  
 Weinstock,G., and Gibbs,R.A.

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## REFERENCE

## AUTHORS

## TITLE

## COMMENT

Submitted (21-MAY-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Nov 20, 2002 this sequence version replaced gi:22656055.  
 The sequence in this assembly is a combination of BAC based reads  
 and whole genome shotgun sequencing reads assembled using Acllas  
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described



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Query Match 31.5%; Score 32.4; DB 9; Length 159598;
Best Local Similarity 62.2%; Pred. NO. 38;
Matches 51; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 5 TGACGGAATAAGCACTTAATGACGCAATTAAGCTCCGATATGGAATGTAATA 64
DB 13823 TCACAGAGATGTCACATGACAGCAAGATTTGCTGTCATCTTTAGCTTCG 138174
OY 65 CAGTTAAATAAAGCGTATTCG 86
DB 138173 CACTTAACACTACATTTTTCG 138152

RESULT 29
AL954648 167153 bp DNA linear HTG 12-MAR-2003
LOCUS Dario rerio clone CH211-245P24, *** SEQUENCING IN PROGRESS ***
DEFINITION unordered pieces.
ACCESSION AL954648
```





Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Glnde, S., Gold, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kells, C., LaRoque, K., Lamazares, R., Landers, T., Lehoczyk, J., Levine, R., Lindblad-Toh, R., Liu, G., Maclean, C., MacDonald, P., Major, J., Marcus, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneses, I., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhkiang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Ribickak, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rossetti, M., Roy, A., Santos, R., Schauer, S., Schoppak, R., Seaman, S., Severy, P., Spencer, B., Stange-Romann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tophan, K., Travers, M., Travis, N., Triggilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.-J., Young, G., Zainoun, J., Zemek, L., Zimmer, A., and Zody, M.

Direct Submission  
Submitted (21-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 22, 2002 this sequence version replaced at:14150949

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
 Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIMR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)  
 Project Information  
 Center project name: L11673  
 Center clone name: 200\_A.13

FEATURES	
source	Location/Qualifiers
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	1925. .2026
repeat_region	/rpt_family="(TA)n"
	2243. .2276
repeat_region	/rpt_family="(CA)n"
	2977. .3023
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	3498. .3614
repeat_region	/rpt_family="L2"
	complement(4068. .4116)
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	4175. .4396
repeat_region	/rpt_family="AluSp"
	complement(4471. .4744)
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	6014. .6056
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	complement(7673. .7976)
repeat_region	/rpt_family="AluSx"
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	complement(9110. .9190)
repeat_region	/rpt_family="MIR3"
	complement(9221. .9531)
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	complement(9749. .9800)
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	complement(9818. .10124)
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	10126. .10199

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repeat_region      /rpt_family="A1uSg"  
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/rpt__family__"TG)n"

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repeat__region
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Query Match	31.5%	Score 32.4;	DB 9;	Length 197877;
Best Local Similarity	62.2%;	Pred. No. 37;		
Matches	51;	Conservative	0;	Mismatches 31;
				Indels 0;
				Gaps 0;

Oy	5	TGATGGAAATAACAGTTTATGTGACAGATTAAAGTCCTCGCATATGTCAATTTGCATAA	64
Dd	42237	TCACTAGAAAGTCCAGTTCACATGACAGCAGAATTTGCTTGTCATCTTTTTAGCTTCG	42296
Oy	65	CAGTTAAAAAACGGTATTTTC	86
Dd	42297	CACTTTAAACCTACATTTTTTC	42318

RESULT 31  
AC069127

LOCUS AC069127 198176 bp DNA linear HTG 01-SEP-2000  
 DEFINITION Homo sapiens chromosome 8 clone RP11-200A13, WORKING DRAFT  
 ACCESSION AC069127  
 VERSION AC069127.1 GI:7923969  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 198176)  
 Waterston, R.H.  
 The sequence of Homo sapiens clone  
 unpublished  
 2 (bases 1 to 198176)  
 Waterston, R.H.  
 Direct Submission  
 Submitted (18-MAY-2000) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA

COMMENT  
 ----- Genome Center -----  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: http://genome.wustl.edu/gsc/index.shtml  
 ----- Project Information -----  
 Center project name: H\_NH0200A13  
 ----- Summary Statistics -----  
 Sequencing vector: pM13; 100%  
 Sequencing vector: plasmid; 0%  
 Chemistry: Dye-terminator Big Dye; 0% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 190387 bases at least Q40  
 Consensus quality: 193248 bases at least Q30  
 Consensus quality: 194812 bases at least Q20  
 Insert size: 188000; agarose-fp  
 Insert size: 196776; sum-of-contigs  
 Quality coverage: 4.45 in Q20 bases; agarose-fp  
 Quality coverage: 4.27 in Q20 bases; sum-of-contigs  
 ----- NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 15 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 1104: contig of 1104 bp in length  
 \* 1105 1204: gap of unknown length  
 \* 1205 2731: contig of 1527 bp in length  
 \* 2732 2831: gap of unknown length  
 \* 2832 7084: contig of 4253 bp in length  
 \* 7085 7184: gap of unknown length  
 \* 7185 10684: contig of 3500 bp in length  
 \* 10685 10784: gap of unknown length  
 \* 10785 16048: contig of 5264 bp in length  
 \* 16049 16148: gap of unknown length  
 \* 16149 21738: contig of 5590 bp in length  
 \* 21739 21838: gap of unknown length  
 \* 21839 27347: contig of 5509 bp in length  
 \* 27348 27447: gap of unknown length  
 \* 27448 33889: contig of 6442 bp in length  
 \* 33890 33989: gap of unknown length  
 \* 33990 50271: contig of 16282 bp in length  
 \* 50272 50371: gap of unknown length  
 \* 50372 66236: contig of 15865 bp in length  
 \* 66237 66336: gap of unknown length  
 \* 66337 85017: contig of 18681 bp in length  
 \* 85018 85117: gap of unknown length  
 \* 85118 103112: contig of 17995 bp in length  
 \* 103113 103212: gap of unknown length

FEATURES  
 source  
 \* 103213 132684: contig of 29472 bp in length  
 \* 132685 132784: gap of unknown length  
 \* 132785 161923: contig of 29139 bp in length  
 \* 161924 162023: gap of unknown length  
 \* 162024 198176: contig of 36153 bp in length.  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="8"  
 /clone="RP11-200A13"  
 1. 1104  
 /note="assembly\_name:Contig14"  
 1205. 2731  
 /note="assembly\_name:Contig15  
 clone\_end:T7  
 vector\_side:left"  
 2832. 7084  
 /note="assembly\_name:Contig18"  
 7185. 10684  
 /note="assembly\_name:Contig19"  
 10785. 16048  
 /note="assembly\_name:Contig20"  
 16149. 21738  
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 21839. 27347  
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 66337. 85017  
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 85118. 103112  
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 103213. 132684  
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 132785. 161923  
 /note="assembly\_name:Contig29"  
 162024. 198176  
 /note="assembly\_name:Contig30"  
 BASE COUNT 62109 a 36068 c 35579 g 63011 t 1409 others  
 ORIGIN  
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 Best Local Similarity 62.2% Pred. No. 37;  
 Matches 51; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
 Oy 5 TGAAGTGAATACGTTTAATGACAGCATTAATGTCGTCATATGTAATGCTATA 64  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 27885 TCACTAAGATGTCGTTCCATGACGACGACAGATTGTCCTGTCATCTTTAGCTCTG 27944  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Oy 65 CAGTTAAAAAAGCGATTTC 86  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 27945 CACTTAAACGTACATTTTCC 27966  
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RESULT 32  
 AL954337/c 205394 bp DNA linear HTG 03-MAY-2003  
 LOCUS AL954337  
 DEFINITION Danio rerio clone CH211-223J10, \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 ACCESSION AL954337  
 VERSION AL954337.7 GI:29786487  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_ACTIVEFIN; HTGS\_DRAFT; HTGS\_FULLTOP.  
 SOURCE Danio rerio (zebrafish)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 205394)  
KAY, M.  
Direct Submission  
Submitted (02-MAY-2003) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
On Apr 10, 2003 this sequence version replaced gi:29561800.  
Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: zfish-help@sanger.ac.uk  
Project Information  
Center project name: zc223j10  
----- Summary Statistics -----  
Assembly program: XGAP4; version 4.5  
Chemistry: Dye-terminator; 99% of reads  
Chemistry: Dye-primer Big Dye; 0% of reads  
Consensus quality: 205262 bases at least Q40  
Consensus quality: 205273 bases at least Q30  
Consensus quality: 205282 bases at least Q20  
Insert size: 205294; sum-of-contigs  
Insert size: 207449; 7.7% error; agarose-fp  
Quality coverage: 10.18x in Q20 bases; sum-of-contigs Quality  
coverage: 10.49x in Q20 bases; agarose-fp  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 2 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\*  
\* 1 4046: contig of 4046 bp in length  
\* 4047 4146: gap of 100 bp  
\* 4147 205394: contig of 201248 bp in length.  
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1. 205394  
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/db\_xref="taxon:7955"  
/clone="CH21-223010"  
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clone\_end:r7  
vector\_side:left"  
4147. 205394  
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misc\_feature  
misc\_feature  
BASE COUNT 64629 a 37468 c 37450 g 65746 t 101 others  
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Best Local Similarity 62.2%; Pred. No. 37;  
Matches 51; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
QY 22 TAATGACAGCATTAATAGCTCTGCTGATATGGAATGCTAATACAGTTAAAAACGTA 81  
DB 194990 TGAATGACAGCTTAATAGCTCTGCTGATATGGAATGCTAATACAGTTAAAAACGTTGATA 194931  
QY 82 TTTCCTGCTGCTGATCAACA 103  
DB 194930 GTTCTGCTGCTGCTGATCAACA 194909  
RESULT 33  
AC021546  
LOCUS AC021546 207756 bp DNA linear PRI 29-JUN-2001

DEFINITION Homo sapiens chromosome 8, clone RP11-57407, complete sequence.  
AC021546  
VERSION AC021546.7 GI:14140331  
KEYWORDS HTG.  
SOURCE  
ORGANISM Homo sapiens (human)  
REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 207756)  
Birren, B., Linton, L., Nussbaum, C. and Lander, E.  
Homo sapiens chromosome 8, clone RP11-57407  
Unpublished  
2 (bases 1 to 207756)  
Birren, B., Linton, L., Nussbaum, C., Lander, E., Abraham, H., Allen, N.,  
Anderson, S., Baldwin, J., Barna, N., Beckley, R., Beda, F.,  
Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G., Castle, A.,  
Chopell, Y., Colangelo, M., Collins, S., Collamore, A., Cooke, P.,  
Dearellano, K., Dewar, K., Domino, M., Doyle, M., Fenesor, J.,  
Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,  
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,  
Howland, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,  
Lander, T., Lechoczky, J., Levine, R., Liu, C., Liu, G., Locke, K.,  
Macdonald, P., Margus, N., McEwan, P., McGurk, A., McKernan, K.,  
McPheeters, R., Meldrum, J., Menus, L., Morrow, J., Naylor, J.,  
Norman, C.H., O'Connor, T., O'Donnell, P., Oliver, T.M., Peterson, K.,  
Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rotman, D.,  
Roy, A., Santos, R., Severy, P., Spencer, P., Stange-Thomann, N.,  
Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,  
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,  
Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 207756)  
Birren, B., Linton, L., Nussbaum, C., Lander, E., Ali, A., Allen, N.,  
Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhalter, B.,  
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,  
Chopell, Y., Colangelo, M., Collins, S., Collamore, A., Cooke, P.,  
Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P.,  
Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S.,  
Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A.,  
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kane, C.,  
Karatas, A., Kells, C., Lacroque, K., Lamares, R., Lander, T.,  
Lechoczky, J., Levine, R., Liu, G., Maclean, C., Macdonald, P., Major, J.,  
Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K.,  
McPheeters, R., Meldrum, J., Menus, L., Mihova, T., Mlenga, V.,  
Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H.,  
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,  
Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,  
Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,  
Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P.,  
Sougnuez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
Strausz, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,  
Topham, K., Travers, M., Travis, N., Trigglio, J., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,  
Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (29-JUN-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On May 17, 2001 this sequence version replaced gi:13518209.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www.seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
Project Information  
Center project name: L5615  
Center clone name: 574\_O\_7  
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Location/Qualifiers

FEATURES

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repeat_region	7510..8455
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35908. .36103
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repeat_region /rpt_family="AluY"
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36251. .36553
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				Gaps 0
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Db	162975	TCACGTAGATGTCATGCATTCATGACAGCAAGATTTCCTTGTCATCTTTTATAGCTTCG	163034	
Qy	65	CAGTTAAAAAAGCGTATTTCC	86	
Db	163035	CACCTTAAACTACATTTTTC	163056	
RESULT 34				
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LOCUS	AC125433	57810 bp	DNA	linear
DEFINITION	Homo sapiens chromosome 11 clone RP11-322L8 map 11, LOW-PASS			
SEQUENCE	SAMPLING.			
ACCESSION	AC125433			

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VERSION      AC125433.1 GI:21591978
KEYWORDS     HTG: HTGS_PHASE0.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
AUTHORS      Birren, B., Nusbaum, C. and Lander, E.
TITLE        Unpublished
JOURNAL      2 (bases 1 to 57810)
REFERENCE    Homo sapiens chromosome 11, clone RP11-322L8
AUTHORS      Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
              Barra, N., Bastien, V., Bloom, F., Boguslavsky, L., Bonkshalter, B.,
              Camarata, J., Chang, J., Chazaro, R., Choepel, Y., Collimore, A.,
              Cook, A., Cooke, P., Dearellano, R., Dewar, K., Diaz, J.S., Dodge, S.,
              Fardo, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
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              Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
              Zemek, L., Zimmer, A. and Zody, M.
              Direct Submission
              Submitted (26-JUN-2002) Whitehead Institute/MIT Center for Genome
              Research, 320 Charles Street, Cambridge, MA 02141, USA
              All repeats were identified using RepeatMasker:
              Smit, A.F.A. & Green, P. (1996-1997)
              http://ftp.genome.washington.edu/RM/RepeatMasker.html
              ----- Genome Center
              Center: Whitehead Institute/ MIT Center for Genome Research
              Center code: WIBR
              Web site: http://www-seq.wi.mit.edu
              Contact: sequence_submissions@genome.wi.mit.edu
              ----- Project Information
              Center project name: L27569
              Center clone name: 322_L_8
              -----
              * NOTE: This record contains 69 individual
              * sequencing reads that have not been assembled into
              * contigs. Runs of N are used to separate the reads
              * and the order in which they appear is completely
              * arbitrary. Low-pass sequence sampling is useful for
              * identifying clones that may be gene-rich and allows
              * overlap relationships among clones to be deduced.
              * However, it should not be assumed that this clone
              * will be sequenced to completion. In the event that
              * the record is updated, the accession number will
              * be preserved.
              *
              1 701: contig of 701 bp in length
              *
              702 801: gap of 100 bp
              *
              802 1571: contig of 770 bp in length
              *
              1572 1671: gap of 100 bp
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              1672 2436: contig of 765 bp in length
              *
              2437 2537: gap of 100 bp
              *
              2537 3244: contig of 708 bp in length
              *
              3245 3344: gap of 100 bp
              *
              3345 4072: contig of 728 bp in length
              *
              4073 4173: gap of 100 bp
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              4173 4921: contig of 749 bp in length
              *
              4922 5021: gap of 100 bp
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              5022 5787: contig of 766 bp in length
              *
              5788 5887: gap of 100 bp
              *
              5888 6642: contig of 755 bp in length
              *
              6643 6742: gap of 100 bp
              *
              6743 7507: contig of 765 bp in length
              *
              7508 7607: gap of 100 bp
              *
              7608 8309: contig of 702 bp in length
              *
              8310 8409: gap of 100 bp
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              8410 9184: contig of 775 bp in length
              *
              9185 9284: gap of 100 bp
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              9285 10041: contig of 757 bp in length
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              10042 10141: gap of 100 bp
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              10141 10887: contig of 746 bp in length
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              10887 10987: gap of 100 bp
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              12661 13407: contig of 747 bp in length
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              13408 13507: gap of 100 bp
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              13508 14240: contig of 733 bp in length
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              15130 15893: contig of 764 bp in length
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              19342 20080: contig of 739 bp in length
              *
              20081 20180: gap of 100 bp
              *
              20181 20907: contig of 727 bp in length
              *
              20908 21007: gap of 100 bp
              *
              21008 21767: contig of 760 bp in length
              *
              21768 21867: gap of 100 bp
              *
              21868 22594: contig of 727 bp in length
              *
              22595 22694: gap of 100 bp
              *
              22695 23454: contig of 760 bp in length
              *
              23455 23554: gap of 100 bp
              *
              23555 24315: contig of 761 bp in length
              *
              24316 24415: gap of 100 bp
              *
              24415 25179: contig of 764 bp in length
              *
              25180 25279: gap of 100 bp
              *
              25280 26030: contig of 751 bp in length
              *
              26031 26130: gap of 100 bp
              *
              26131 26876: contig of 746 bp in length
              *
              26877 26976: gap of 100 bp
              *
              26976 27730: contig of 754 bp in length
              *
              27731 27830: gap of 100 bp
              *
              27831 28582: contig of 752 bp in length
              *
              28583 28682: gap of 100 bp
              *
              28683 29438: contig of 756 bp in length
              *
              29439 29538: gap of 100 bp
              *
              29539 30303: contig of 765 bp in length
              *
              30304 30403: gap of 100 bp
              *
              30404 31087: contig of 684 bp in length
              *
              31088 31187: gap of 100 bp
              *
              31188 31950: contig of 763 bp in length
              *
              31951 32050: gap of 100 bp
              *
              32051 32799: contig of 749 bp in length
              *
              32800 32899: gap of 100 bp
              *
              32900 33649: contig of 750 bp in length
              *
              33650 33749: gap of 100 bp
              *
              33750 34462: contig of 713 bp in length
              *
              34463 34562: gap of 100 bp
              *
              34563 35306: contig of 744 bp in length
              *
              35307 35406: gap of 100 bp
              *
              35407 36149: contig of 743 bp in length
              *
              36150 36249: gap of 100 bp
              *
              36250 37003: contig of 754 bp in length
              *
              37004 37103: gap of 100 bp
              *
              37104 37872: contig of 769 bp in length
              *
              37873 38703: contig of 731 bp in length
              *

```

```

*      38704      38803: gap of 100 bp
*      38804      39565: contig of 762 bp in length
*      39566      39665: gap of 100 bp
*      39666      40426: contig of 761 bp in length
*      40427      40526: gap of 100 bp
*      40527      41264: contig of 738 bp in length
*      41265      41364: gap of 100 bp
*      41365      42088: contig of 724 bp in length
*      42089      42188: gap of 100 bp
*      42189      42924: contig of 736 bp in length
*      42925      43024: gap of 100 bp
*      43025      43751: contig of 727 bp in length
*      43752      43851: gap of 100 bp
*      43852      44616: contig of 765 bp in length
*      44617      44716: gap of 100 bp
*      44717      45476: contig of 760 bp in length
*      45477      45576: gap of 100 bp
*      45577      46341: contig of 765 bp in length
*      46342      46441: gap of 100 bp
*      46442      47113: contig of 672 bp in length
*      47114      47213: gap of 100 bp
*      47214      47919: contig of 706 bp in length
*      47920      48019: gap of 100 bp
*      48020      48785: contig of 766 bp in length
*      48786      48885: gap of 100 bp
*      48886      49563: contig of 684 bp in length
*      49570      49669: gap of 100 bp
*      49670      50374: contig of 705 bp in length
*      50375      50474: gap of 100 bp
*      50475      51197: contig of 723 bp in length
*      51198      51297: gap of 100 bp
*      51298      52033: contig of 736 bp in length
*      52034      52133: gap of 100 bp
*      52134      52895: contig of 762 bp in length
*      52896      52995: gap of 100 bp
*      52996      53697: contig of 702 bp in length
*      53698      53797: gap of 100 bp
*      53798      54446: contig of 649 bp in length
*      54447      54546: gap of 100 bp
*      54547      55284: contig of 738 bp in length
*      55285      55384: gap of 100 bp
*      55385      56119: contig of 735 bp in length
*      56120      56219: gap of 100 bp
*      56220      56968: contig of 750 bp in length
*      56970      57069: gap of 100 bp
*      57070      57810: contig of 741 bp in length.

```

```

FEATURES
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    /mol_type="genomic DNA"

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Query Match      31.1%; Score 32; DB 2; Length 57810;
Best Local Similarity 58.3%; Pred. No. 55;
Matches 56; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

```

```

Oy      3 AGTCACGCGAATTAACATTTAATGACAGCATTAATAGCTCTCGATATGTAATGCTAA 62
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      14752 AGTAGCTGGAGCAACAGCATGTCACACTCTACTATGTTTTTAAATTTTAA 14693
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy      63 TACAGTTAAATAAAGGTAATTCCTGGTGTCTGATC 98
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      14692 TAGAGATGAGGTCTCATTAATTTTCCCAAGGCTGATC 14657
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 35
AC104655/c      95616 bp      DNA      Linear      PRI 21-FEB-2002
LOCUS      AC104655
DEFINITION      Homo sapiens BAC clone RP11-383P6 from 2, complete sequence.
ACCESSION      AC104655
VERSION      AC104655.4      GI:18482325
KEYWORDS      HTG.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens

```

```

REFERENCE
AUTHORS      Sulston, J.E. and Waterston, R.
TITLE      Toward a complete human genome sequence
JOURNAL      Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE      99063792
PUBMED      9847074
REFERENCE
AUTHORS      Tomlinson, C. and Cotton, M.
TITLE      The sequence of Homo sapiens BAC clone RP11-383P6
JOURNAL      Unpublished (2001)
REFERENCE
AUTHORS      Waterston, R.H.
TITLE      Direct Submission
JOURNAL      Submitted (18-DEC-2001) Genome Sequencing Center, Washington
              University School of Medicine, 4444 Forest Park Parkway, St. Louis,
              MO 63108, USA
              4 (bases 1 to 95616)
REFERENCE
AUTHORS      Waterston, R.H.
TITLE      Direct Submission
JOURNAL      Submitted (03-FEB-2002) Genome Sequencing Center, Washington
              University School of Medicine, 4444 Forest Park Parkway, St. Louis,
              MO 63108, USA
              5 (bases 1 to 95616)
REFERENCE
AUTHORS      Waterston, R.
TITLE      Direct Submission
JOURNAL      Submitted (21-FEB-2002) Department of Genetics, Washington
              University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
              On Feb 3, 2002 this sequence version replaced gi.18308880.
COMMENT
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: saplens@watson.wustl.edu
----- Summary Statistics -----
Center project name: H_NH0383P06

```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

#### MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

#### SOURCE INFORMATION:

The RP11-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P. Y., Zhao, B., Frenken, E., Tatenno, M., Catanesi, J. J., and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org> VECTOR: pBACe3.6

#### NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-653B19; the clone sequenced to the right is RP11-332H14. Actual start of this clone is at base position 1 of RP11-383P6.

Polymorphisms have been identified between AC104655 and AC012360.  
Data from AC107080 was used to finish this clone, AC104655.

## FEATURES

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        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"
        /chromosome="2"
        /map="2"
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        /clone_11b="RP11-11"
        18. 67
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    390. 519
repeat_region
    /rpt_family="L1"
    520. 820
repeat_region
    /rpt_family="Alu"
    821. 882
repeat_region
    /rpt_family="L1"
    885. 1131
repeat_region
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    1269. 1647
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    1691. 1719
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    /rpt_family="AT-rich"
    1703. 1861
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    /rpt_family="TC2"
    1865. 1890
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    /rpt_family="(TG)n"
    2466. 2652
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    3525. 3635
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    /note="match to EST BI489887 (NID:g15329115)"
    3525. 3611
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    3525. 3611
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    3525. 3611
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    3525. 3611
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    3525. 3611
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    /note="match to EST BI834044 (NID:g15945594)"
    3526. 3635
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    3530. 3611
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    3530. 3611
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    3533. 3604
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    4004. 4024
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    7797. 7821
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    /rpt_family="(TA)n"
    9686. 9752
repeat_region
    /rpt_family="MIR"
    9697. 9846
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    10932. 11013
repeat_region
    /rpt_family="MER1_type"
    10966. 11294
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    /note="match to EST AA569191 (NID:g2342245) nm30e04.s1"
    11105. 11144
repeat_region
    /rpt_family="T-rich"
    11323. 11383
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    11385. 11611

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```

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    /rpt_family="MER1_type"
    12059. 12081
repeat_region
    /rpt_family="AT-rich"
    12527. 12618
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    /note="match to EST BI490606 (NID:g15329834)"
    12531. 12618
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    /note="match to EST BI489771 (NID:g15328999)"
    12533. 12618
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    /note="match to EST AL561150 (NID:g12908295)"
    12533. 12618
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    /note="match to EST BE093631 (NID:g8484083)"
    12533. 12618
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    /note="match to EST BE787502 (NID:g10208622)"
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    /note="match to EST BI834044 (NID:g15945594)"
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    12533. 12572
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    12552. 12601
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    12601. 12618
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    12918. 12948
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    13445. 13544
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    /note="similar to Mus musculus EST AA110469 (NID:g1662228) m61h05.r1"
    13445. 13544
misc_feature
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misc_feature
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    13466. 13544
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    /note="similar to Mus musculus EST BF181151 (NID:g11059293)"
    13466. 13544
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    /note="similar to Rattus norvegicus EST BF551841 (NID:g11661571)"
    13469. 13548
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    /note="match to EST BI834044 (NID:g15945594)"
    13469. 13548

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Query Match 31.1%; Score 32; DB 9; Length 95616;  
Best Local Similarity 62.5%; Pred. No. 52;  
Matches 50; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

```

QY 17 CAGTTTATGACAGCATTAATAGCTTCGCATATGTAATTCCTAATACAGTTAAAAA 76
    ||||| ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 44539 CAGTTGATGAAGAAGTAATAGCTGAGAAATGTAATGATGATGACACAAATAAAC 44480
QY 77 CGGTAATCCCGGTTCTGA 96
    || ||||| ||||| || ||||| || ||||| || ||||| || |||||
Db 44479 AAGTTGTCATGCGCCCTAA 44460

```

RESULT 36  
AC026733/C 132120 bp DNA 1linear PRI 15-AUG-2001  
DEFINITION Homo sapiens chromosome 5 clone CTD-2325018, complete sequence.  
ACCESSION AC026733  
VERSION AC026733.5 GI:15187255  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 132120)





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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RP11-2621"
/clone_lib="RPC1-11 Human Male BAC"
1. 10149
/misc_feature
  /note="assembly_fragment"
  clone_end:SP6
  vector_side:left"
misc_feature
  /note="assembly_fragment"
  10250..11394
misc_feature
  /note="assembly_fragment"
  11495..14270
misc_feature
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  28040..34728
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  34829..42086
misc_feature
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  42187..50072
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  75359..92799
misc_feature
  /note="assembly_fragment"
  92900..120162
misc_feature
  /note="assembly_fragment"
  120263..157331
BASE COUNT 51730 a 27082 c 27663 g 49552 t 1304 others
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Query Match 31.1%; Score 32; DB 2; Length 157331;
Best Local Similarity 58.3%; Pred. No. 49;
Matches 56; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 2 AAGTACGTGAGATACAGTTTATGACGATTAATAGCTCCTGCATATGCAATGCTCA 61
DB 153428 AATAGTATGCTTCATTAATATGACAAAGTATTAGCCCATTAATATGTTCTTACAA 153369
QY 62 ATACAGTTAAAAAAGCGATTTCCTGCTGCTGAT 97
DB 153368 CAGAGGCTCTATTATGCTTTTCCATCTTACTGAT 153333
RESULT 38
AC103561 172387 bp DNA linear HTG 29-NOV-2001
LOCUS AC103561
DEFINITION Homo sapiens chromosome UNK clone RP11-381012, *** SEQUENCING IN
PROGRESS ***, 29 unordered pieces.
ACCESSION AC103561
VERSION AC103561.1 GI:17136164
KEYWORDS HTG; HTGS; PHASE1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 172387)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 172387)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (28-NOV-2001) Genome Sequencing Center, Washington
UNIVERSITY School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
```

## COMMENT

```
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0381012
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 159141 bases at least Q40
Consensus quality: 162137 bases at least Q30
Consensus quality: 164330 bases at least Q20
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 29 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
1445: contig of 1445 bp in length
1446 1445: gap of unknown length
1546 3325: contig of 1680 bp in length
3326 3325: gap of unknown length
3326 4999: contig of 1674 bp in length
5000 5099: gap of unknown length
5100 6668: contig of 1569 bp in length
6669 6768: gap of unknown length
6769 9126: contig of 2358 bp in length
9127 9226: gap of unknown length
9227 11622: contig of 2396 bp in length
11623 11722: gap of unknown length
11723 14397: contig of 2675 bp in length
14398 14497: gap of unknown length
14498 17393: contig of 2896 bp in length
17394 17493: gap of unknown length
17494 19681: contig of 2188 bp in length
19682 19781: gap of unknown length
19782 21624: contig of 1843 bp in length
21625 21724: gap of unknown length
21725 24150: contig of 2426 bp in length
24151 24250: gap of unknown length
24251 26778: contig of 2528 bp in length
26779 26878: gap of unknown length
26879 29564: contig of 2686 bp in length
29565 29664: gap of unknown length
29665 34209: contig of 4545 bp in length
34210 34309: gap of unknown length
34310 36982: contig of 2673 bp in length
36983 37082: gap of unknown length
37083 41009: contig of 3927 bp in length
41010 41109: gap of unknown length
41110 44807: contig of 3698 bp in length
44808 44907: gap of unknown length
44908 49781: contig of 4874 bp in length
49782 49881: gap of unknown length
49882 56837: contig of 6956 bp in length
56838 63920: contig of 6983 bp in length
63921 64020: gap of unknown length
64021 72339: contig of 8319 bp in length
72340 72439: gap of unknown length
72440 79950: contig of 7511 bp in length
79951 80050: gap of unknown length
80051 87496: contig of 7446 bp in length
87497 87596: gap of unknown length
87597 102735: contig of 15139 bp in length
102736 102835: gap of unknown length
```



```

Sequencing vector: M13: M77815: 16% of reads
Sequencing vector: Plasmid: n/a: 84% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 186043 bases at least Q40
Consensus quality: 188508 bases at least Q30
Consensus quality: 189610 bases at least Q20
Insert size: 180000; agarose-fp
Insert size: 190382; sum-of-contigs
Quality coverage: 5.9 in Q20 bases; agarose-fp
Quality coverage: 5.6 in Q20 ba.
NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 17288: contig of 17288 bp in length
17289 17388: gap of 100 bp
17389 18865: contig of 1477 bp in length
18866 18965: gap of 100 bp
18966 20267: contig of 1302 bp in length
20268 20367: gap of 100 bp
20368 23131: contig of 2764 bp in length
23132 23232: gap of 100 bp
23232 25413: contig of 2182 bp in length
25414 25513: gap of 100 bp
25514 34595: contig of 9082 bp in length
34596 43265: gap of 100 bp
43266 43365: gap of 100 bp
43366 51536: contig of 8171 bp in length
51537 85136: gap of 100 bp
85137 85831: contig of 34095 bp in length
85832 103757: gap of 100 bp
103758 103857: gap of 100 bp
103858 125710: contig of 21853 bp in length
125711 125810: gap of 100 bp
125811 147528: contig of 21718 bp in length
147529 147628: gap of 100 bp
147629 173985: contig of 26357 bp in length
173986 174086: gap of 100 bp
174086 191682: contig of 17597 bp in length.
*
FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
/map="2"
/clone_id="RP11-61701"
/clone_lib="RPCT-11 Human Male BAC"
1..17288
/feature="assembly_fragment"
clone_end:sp6
vector_side:left"
17389..18865
/feature="assembly_fragment"
18966..20267
/feature="assembly_fragment"
20368..23131
/feature="assembly_fragment"
23232..25413
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25514..34595
/feature="assembly_fragment"
34696..43265
/feature="assembly_fragment"
43366..51536
/feature="assembly_fragment"
51537..85136
/feature="assembly_fragment"
85137..103757
/feature="assembly_fragment"
103758..103857
/feature="assembly_fragment"
103858..125710
/feature="assembly_fragment"
125711..125810
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125811..147528
/feature="assembly_fragment"
147529..147628
/feature="assembly_fragment"
147629..173985
/feature="assembly_fragment"
173986..174086
/feature="assembly_fragment"
174087..191682
/feature="assembly_fragment"

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                  /note="assembly-fragment"
misc_feature      85832..103757
                  /note="assembly-fragment"
misc_feature      103858..125710
                  /note="assembly-fragment"
misc_feature      125811..147528
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misc_feature      147629..173985
                  /note="assembly-fragment"
misc_feature      174086..191682
                  /note="assembly-fragment"
                  clone_end:T7
                  vector_side:right"

BASE COUNT      57363 a 37778 c 38363 g 56876 t 1302 others
ORIGIN

Query Match      31.1%; Score 32; DB 2; Length 191682;
Best Local Similarity 62.5%; Pred. No. 48;
Matches 50; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

OY      17 CAGTTAATGACAGCATTAAATGATCCGTCATGTAATGCTAATACAGTAAAAAAA 76
          ||||| ||||| || ||||| || ||||| || ||||| || |||||
Db      106077 CAGTTGATGAAGAAGTAATAGCGTCGAGAAATGTGATGATGATGATCAACAATTAAC 106018
          || ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY      77 CGGTATTTCCCTGCTCTGA 96
          || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      106017 AAGTTTGTCATGCGCCCTAA 105998

RESULT 40
BX469936/c      214165 bp DNA linear HTG 02-MAY-2003
DEFINITION      Danio rerio clone DKEX-32112, *** SEQUENCING IN PROGRESS ***, 22
LOCUS           BX469936
ACCESSION       BX469936
VERSION         BX469936.2 GI:30348675
KEYWORDS        HTG; HTGS-PHASE1.
SOURCE          Danio rerio (zebrafish)
ORGANISM        Danio rerio
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
                Cypriniformes; Cyprinidae; Danio.
                1 (bases 1 to 214165)
                Sims,S.
                Direct Submission
                Submitted (01-May-2003) Wellcome Trust Sanger Institute, Hinxton,
                Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                On May 2, 2003 this sequence version replaced gi:30142560.
                ----- Genome Center
                Center: Wellcome Trust Sanger Institute
                Center code: SC
                Web site: http://www.sanger.ac.uk
                Contact: zfish-help@sanger.ac.uk
                Project Information
                Center project name: zK32112
                ----- Summary Statistics
                Assembly program: XCAP4; version 4.5
                Chemistry: Dye-terminator; 100% of reads
                Consensus quality: 204770 bases at least Q40
                Consensus quality: 206594 bases at least Q30
                Consensus quality: 208843 bases at least Q20
                Insert size: 212065; sum-of-ctrls
                Insert size: 210479; 9.8% error; agarose-fp
                Quality coverage: 4.59x in Q20 bases; sum-of-ctrls quality
                coverage: 4.81x in Q20 bases; agarose-fp
                -----
                * NOTE: This is a 'working draft' sequence. It currently
                * consists of 22 contigs. The true order of the pieces
                * is not known and their order in this sequence replaced is
                * arbitrary. Gaps between the contigs are represented as
                * runs of N, but the exact sizes of the gaps are unknown.

```

```

ures
source
    location/Qualifiers
    1. .214165
        /organism="Danio rerio"
        /mol_type="genomic DNA"
        /db_xref="taxon:7955"
        /clone="DK97-32112"
        /clone_id="Daniokey"
        1..3151
misc-feature
    /note="assembly-fragment:01542"
    fragment_chain:1"
    3252..17528
misc-feature
    /note="assembly-fragment:017000"
    fragment_chain:1"
    17629..22436
misc-feature
    /note="assembly-fragment:01569"
    fragment_chain:1"
    22537..29137
misc-feature
    /note="assembly-fragment:01410"
    fragment_chain:1"
    29474..51943
misc-feature
    /note="assembly-fragment:016000"
    fragment_chain:1"
    52044..56035
misc-feature
    /note="assembly-fragment:00560"
    fragment_chain:1"
    56136..80706
misc-feature
    /note="assembly-fragment:01101"

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Query Match	30.98;	Score 31.8;	DB 2;	Length 214165;
Best Local Similarity	57.6%;	Pred. No. 53;		
Matches 57; Conservative	0;	Mismatches 42;	Indels 0;	Gaps 0;

  

Oy	5	TGACGTGAATAACAGCTTAATGACACCATTAATAGCCTCGCATGATGAAATTGCATAA	64
Db	87811	TCACATCTCTCAACACTTTGGATTAACAAGTAAAAAGAACAATCCAGTTCAAAATTA	CTTTT 87752
Oy	65	CAGTTAAAAAACGGTATTTCCCTCGGTGTCGATCCACA	103
Db	87751	ATGTTAAAAATACATAATTTTTCAGGGTTTTTTTTCACCA	87713

  

RESULT 41	
AC097421/c	
LOCUS	248948 bp DNA linear HTG 10-MAY-2003
DEFINITION	Rattus norvegicus clone CH230-24E11, *** SEQUENCING IN PROGRESS
ACCESSION	AC097421
VERSION	AC097421.6 GI:30521335
KEYWORDS	HTG; HTGS PHASE1; HTGS_DRAPI; HTGS_ENRICHED.
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.





TITLE Direct Submission  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 448185)  
AUTHORS Worley, K.C.  
JOURNAL Direct Submission  
Submitted (14-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 448185)  
Rat Genome Sequencing Consortium.  
Submitted (12-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Oct 12, 2002 this sequence version replaced gi:21465216.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: KA02  
Center clone name: CH230-486P3  
----- Summary Statistics  
Assembly program: Phrap; version 0.990329  
Consensus quality: 355484 bases at least Q40  
Consensus quality: 369229 bases at least Q30  
Consensus quality: 376812 bases at least Q20  
Estimated insert size: 496298; sum-of-contigs estimation  
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_craft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_craft_data.html))  
\* NOTE: This sequence may represent more than one clone.  
\* NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 26070: contig of 26070 bp in length  
\* 26071 26170: gap of unknown length  
\* 26171 83555: contig of 57485 bp in length  
\* 83556 83755: gap of unknown length  
\* 83756 98687: contig of 14932 bp in length  
\* 98688 98787: gap of unknown length  
\* 98788 119532: contig of 20745 bp in length  
\* 119533 119632: gap of unknown length  
\* 119633 130323: contig of 10691 bp in length  
\* 130324 130423: gap of unknown length  
\* 130424 158608: contig of 28185 bp in length  
\* 158609 158708: gap of unknown length  
\* 158709 169812: contig of 11104 bp in length  
\* 169813 169912: gap of unknown length  
\* 169913 201720: contig of 31808 bp in length  
\* 201721 201820: gap of unknown length  
\* 201821 217149: contig of 15329 bp in length  
\* 217150 217249: gap of unknown length  
\* 217250 244384: contig of 27135 bp in length

244385 244484: gap of unknown length  
\* 244485 248149: contig of 3665 bp in length  
\* 248150 248249: gap of unknown length  
\* 248250 253526: contig of 5277 bp in length  
\* 253527 253626: gap of unknown length  
\* 253627 266141: contig of 12514 bp in length  
\* 266141 266240: gap of unknown length  
\* 266241 284166: contig of 17926 bp in length  
\* 284167 284266: gap of unknown length  
\* 284267 288035: contig of 3769 bp in length  
\* 288036 288135: gap of unknown length  
\* 288136 351975: contig of 63840 bp in length  
\* 351976 352075: gap of unknown length  
\* 352076 356720: contig of 4645 bp in length  
\* 356721 356820: gap of unknown length  
\* 356821 367631: contig of 10811 bp in length  
\* 367632 367731: gap of unknown length  
\* 367732 388952: contig of 21221 bp in length  
\* 388953 389052: gap of unknown length  
\* 389053 390382: contig of 1330 bp in length  
\* 390383 390482: gap of unknown length  
\* 390483 394515: contig of 4033 bp in length  
\* 394516 394615: gap of unknown length  
\* 394616 400601: contig of 5966 bp in length  
\* 400602 400701: gap of unknown length  
\* 400702 410562: contig of 9861 bp in length  
\* 410563 410662: gap of unknown length  
\* 410663 416153: contig of 5491 bp in length  
\* 416154 416253: gap of unknown length  
\* 416254 448185: contig of 31932 bp in length.

FEATURES  
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1..448185 Location/Qualifiers  
1..448185 **organism**="Rattus norvegicus"  
1..448185 **mol\_type**="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-486P3"  
1..4191  
/note="wgs\_end-extension  
clone\_end:Sp6"  
6779..7355  
/note="clone boundary  
clone\_end:Sp6  
site:Mbol  
end\_sequence:RXBQM86TY"  
14709..18698  
/note="wgs\_contig"  
19740..26070  
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26171..27385  
/note="wgs\_contig"  
32433..41624  
/note="wgs\_contig"  
42273..44529  
/note="wgs\_contig"  
44580..48089  
/note="wgs\_contig"  
48484..51371  
/note="wgs\_contig"

Query Match 30.7%; Score 31.6; DB 2; Length 110000;  
Best Local Similarity 74.1%; Pred. No. 65;  
Matches 40; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
OY 32 ATTAAAGCCTCGCATATGTAATTCGTAATGACAGTTAAAAACGTAATTC 85  
||||| ||| ||||| ||||| ||| ||| ||| ||||| |||||  
DB 74161 ATTACTAGAGCCTGCTTATGTGTAACACTACAGAACTCTCAAGAAAACAGTATTC 74108

Search completed: August 25, 2003, 07:22:02  
Job time : 1605 secs



Result No.	Score	Query Match	Length	DB	ID	Description
C 1	36.2	35.1	74962	4	US-09-685-853A-3	Sequence 3, Appl1
C 2	29.2	28.3	148567	4	US-09-801-876B-3	Sequence 3, Appl1
C 3	28.8	28.0	1830121	4	US-09-557-884-1	Sequence 1, Appl1
C 4	28.8	28.0	1830121	4	US-09-643-990A-1	Sequence 1, Appl1
C 5	28.4	27.6	2692	4	US-09-453-702B-215	Sequence 215, App
C 6	28	27.2	466	4	US-09-996-243-106	Sequence 106, App
C 7	27.6	26.8	170	3	US-08-981-601-26	Sequence 26, Appl
C 8	27.6	26.8	1070	2	US-08-179-557-17	Sequence 17, Appl
9	27.6	26.8	2581	1	US-08-200-900A-1	Sequence 1, Appl1
10	27.6	26.8	2581	5	PCR-US84-00616-1	Sequence 1, Appl1
11	27.6	26.8	3054	4	US-09-484-970B-138	Sequence 138, App
12	27.4	26.6	3001	4	US-09-539-333D-196	Sequence 196, App
13	27.4	26.6	5508	4	US-09-220-133-2	Sequence 2, Appl1
14	27.4	26.6	11485	4	US-09-410-464-9	Sequence 9, Appl1
C 15	27.4	26.6	2020001	4	US-09-734-674-3	Sequence 3, Appl1
C 16	27.2	26.4	306	4	US-09-328-352-1715	Sequence 1715, App
C 17	27.2	26.4	325	4	US-09-601-195-108	Sequence 108, App
C 18	27.2	26.4	4946	3	US-08-930-996A-1	Sequence 1, Appl1
C 19	27	26.2	1287	4	US-09-328-335-1417	Sequence 1417, Ap
20	26.8	26.0	5398	3	US-09-356-955-11	Sequence 11, Appl
C 21	26.8	26.0	98844	4	US-09-791-211-10	Sequence 10, Appl
C 22	26.8	26.0	1830121	4	US-09-557-884-1	Sequence 1, Appl1
C 23	26.8	26.0	1830121	4	US-09-643-990A-1	Sequence 1, Appl1
C 24	26.6	25.8	1038	1	US-08-680-726A-53	Sequence 53, Appl
C 25	26.6	25.8	1038	3	US-09-092-409-53	Sequence 53, Appl
C 26	26.6	25.8	1330	1	US-08-220-151-18	Sequence 18, Appl
C 27	26.6	25.8	1330	1	US-08-413-118-18	Sequence 18, Appl

C 28	26.6	25.8	1.120	3	US-08-473-448-18	Sequence 18, Appl
C 29	26.6	25.8	1.115	1	US-08-411-3-116-126	Sequence 126, Appl
C 30	26.6	25.8	1.145	3	US-08-473-446-126	Sequence 126, Appl
C 31	26.6	25.8	1.0592	1	US-08-680-7266-51	Sequence 51, Appl
C 32	26.6	25.8	1.0592	1	US-08-680-7266-52	Sequence 52, Appl
C 33	26.6	25.8	1.0592	3	US-09-092-409-51	Sequence 51, Appl
C 34	26.6	25.8	1.0592	3	US-09-092-409-52	Sequence 52, Appl
C 35	26.6	25.6	4.94	4	US-09-702-705-655	Sequence 655, Appl
C 36	26.6	25.6	4.94	4	US-09-736-457-655	Sequence 655, Appl
C 37	26.2	25.4	1.993	4	US-09-107-5326-3072	Sequence 3072, Appl
C 38	26.2	25.4	6.350	4	US-09-647-826-1	Sequence 1, Appl1
C 39	26	25.2	4.90	4	US-09-596-243-105	Sequence 105, Appl
C 40	25.8	25.0	2.97	4	US-08-616-368-17	Sequence 17, Appl
C 41	25.8	25.0	2.97	3	US-09-054-298-17	Sequence 17, Appl
C 42	25.8	25.0	2.97	3	US-08-818-655-17	Sequence 17, Appl
C 43	25.8	25.0	2.97	4	US-09-305-839-17	Sequence 17, Appl
C 44	25.8	25.0	5.45	4	US-09-996-243-104	Sequence 104, Appl
C 45	25.8	25.0	5.45	4	US-09-996-243-108	Sequence 108, Appl

## ALIGNMENTS

```

RESULT 1
US-09-685-853A-3/C
; Sequence 3, Application US/09685853A
; Patent No. 6479270
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CLO00871
; CURRENT APPLICATION NUMBER: US/09/685,853A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/182,194
; PRIOR FILING DATE: 2000-02-14
; NUMBER OF SEQ. ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 74962
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(74962)
; OTHER INFORMATION: n = A,T,C or G
US-09-685-853A-3

Query Match          35.1%  Score 36.2:  DB 4:  Length 74962;
Best local similarity 62.9%:  Pred. No. 0.018;
Matches 56; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY      12 AATAACGATTAAATGACAGCATTTAATAGCTCTGCATATGTGAATTCCTAATACAGTTAA 71
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db      63338 AAAAAAATTCAGACTTCAAGACCCCTAGACACTTACTTTCTATCATCAATTAA 63279
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
QY      72 AAAAAAGGTATTTCCCTGGTTCTGATCCA 100
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db      63278 AAAAAAGTCTTCAGTACTTCATCTCA 63250
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

RESULT 2
US-09-801-876B-3/C
; Sequence 3, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01160
; CURRENT APPLICATION NUMBER: US/09/801,876B

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;; CURRENT FILING DATE: 2001-03-09  
;; NUMBER OF SEQ ID NOS: 8  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO: 3  
;; LENGTH: 148567  
;; TYPE: DNA  
;; ORGANISM: Human  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)...(148567)  
;; OTHER INFORMATION: n = A,T,C or G  
US-09-801-876B-3

Query Match 28.3%; Score 29.2; DB 4; Length 148567;  
Best Local Similarity 56.1%; Pred. No. 4;  
Matches 55; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 5 TGACGGAATAACGTTTAATGACAGCAATTAATAGCTCTGCATATGTAATGCTAATA 64  
DB 73665 TGCATTGCAATTATATGTAATGACCAATTAATATTTCTTTGGCTGAATTGCTCACT 73626  
QY 65 CAGTTAAAAAAGCGTATTTCCCTGGTCTGATCCAC 102  
DB 73625 AATTGACAAAGATTCTGTGCGCTGCTCATTTCTAC 73588

## RESULT 3

US-09-557-884-1/c  
; Sequence 1, Application US/09557884  
; Patent No. 6506581

## GENERAL INFORMATION:

APPLICANT: Fleischmann et al.

TITLE OF INVENTION: The Nucleotide sequence of  
the Haemophilus influenzae Rd Genome, Fragments  
Thereof, and Uses Thereof

## NUMBER OF SEQUENCES: 1

## CORRESPONDENCE ADDRESS:

ADDRESS: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: MD

COUNTRY: USA

ZIP: 20850

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/557,884

FILING DATE: 25-Apr-2000

CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/476,102

FILING DATE: JUN-5-1995

ATTORNEY/AGENT INFORMATION:

NAME: Michelle S. Marks

REGISTRATION NUMBER: 41,971

REFERENCE/DOCKET NUMBER: PB186P3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1830121 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-557-884-1

Query Match 28.0%; Score 28.8; DB 4; Length 1830121;  
Best Local Similarity 58.0%; Pred. No. 9.8;

Matches 51; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 13 ATAACAGTTTAATGACAGCAATTAATAGCTCTGCATATGTAATGCTAATACAGTTAAA 72

DB 1541231 ATTAAGAGTCGTTATTTCCATTAATAGTTAGTGAATGTAATTTCCATTTCATTTAAT 1541172

QY 73 AAAACGGTATTTCCCTGGTCTGATCCA 100

DB 1541171 AAAAATATAATTCCTCATTCATCCCA 1541144

## RESULT 4

US-09-643-990A-1/c  
; Sequence 1, Application US/09643990A  
; Patent No. 6528289

## GENERAL INFORMATION:

APPLICANT: Robert D. Fleischmann

Mark D. Adams

Owen White

Hamilton O. Smith

J. Craig Venter

TITLE OF INVENTION: The Nucleotide sequence of  
the Haemophilus influenzae Rd Genome, Fragments  
Thereof, and Uses Thereof

## NUMBER OF SEQUENCES: 1

## CORRESPONDENCE ADDRESS:

ADDRESS: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville,

STATE: MD

COUNTRY: USA

ZIP: 20850

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/643,990A

FILING DATE: 23-Aug-2000

CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/487,429

FILING DATE: 1995-06-07

APPLICATION NUMBER: 08/426,787

FILING DATE: 1995-04-21

ATTORNEY/AGENT INFORMATION:

NAME: Kenley K. Hoover

REGISTRATION NUMBER: 40,302

REFERENCE/DOCKET NUMBER: PB186P1C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-610-5790

TELEFAX: 310-309-8439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1830121 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-643-990A-1

Query Match 28.0%; Score 28.8; DB 4; Length 1830121;  
Best Local Similarity 58.0%; Pred. No. 9.8;  
Matches 51; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 13 ATAACAGTTTAATGACAGCAATTAATAGCTCTGCATATGTAATGCTAATACAGTTAAA 72

DB 1541231 ATTAAGAGTCGTTATTTCCATTAATAGTTAGTGAATGTAATTTCCATTTCATTTAAT 1541172

QY 73 AAAACGGTATTTCCCTGGTCTGATCCA 100

DB 1541171 AAAAATATAATTCCTCATTCATCCCA 1541144

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RESULT 5
US-09-453-7028-215/c
; Sequence 215, Application US/094537028
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Valerie
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,7028
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-Dec-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296,95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 215:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2692
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 215:
US-09-453-7028-215

Query Match      27.6% Score 28.4; DB 4; Length 2692;
Best Local Similarity 54.9%; Pred. No. 2.8;
Matches 56; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 2 AAGTGAAGTGAATACAGTTAATGACAGCATTAATGCTCTGATATGTAATGCTA 61
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1129 ACGTGAATGACGATGATTTATTTATTTGCAAGAAATGAAGAACTAGCAAAATGTTTCCCTT 1070
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 62 ATACAGTTAAAAAACGCTATTTCCCTGCTTCGATCCACA 103
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1069 TTTTGGACATATATAAAACACTTATCGAAGATCGATGACAA 1028
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
US-09-996-243-106/c
; Sequence 106, Application US/09996243
; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
```

```
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsens, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C13
; CURRENT APPLICATION NUMBER: US/09/996,243
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
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: PRIOR APPLICATION NUMBER: 60/090445
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090472
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090535
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090540
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090542
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090557
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090676
: PRIOR FILING DATE: 1998-06-25
: PRIOR APPLICATION NUMBER: 60/090678
: PRIOR FILING DATE: 1998-06-25
: PRIOR APPLICATION NUMBER: 60/090690
: PRIOR FILING DATE: 1998-06-25
: PRIOR APPLICATION NUMBER: 60/090694
: PRIOR FILING DATE: 1998-06-25
: PRIOR APPLICATION NUMBER: 60/090695
: PRIOR FILING DATE: 1998-06-25
: PRIOR APPLICATION NUMBER: 60/090696
: PRIOR FILING DATE: 1998-06-25
: PRIOR APPLICATION NUMBER: 60/090862
: PRIOR FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: 60/090863
: PRIOR FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: 60/091360
: PRIOR FILING DATE: 1998-07-01
: PRIOR APPLICATION NUMBER: 60/091478
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091544
: PRIOR FILING DATE: 1998-07-01
: PRIOR APPLICATION NUMBER: 60/091519
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091626
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091633
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091978
: PRIOR FILING DATE: 1998-07-07
: PRIOR APPLICATION NUMBER: 60/091982
: PRIOR FILING DATE: 1998-07-07
: PRIOR APPLICATION NUMBER: 60/092182
: PRIOR FILING DATE: 1998-07-09

Query Match      27.2%; Score 28; DB 4; Length 466;
Best Local Similarity 59.7%; Pred. No. 2.4;
Matches 46; Conservative 0; Mismatches 31; IndeIs 0; Gaps 0;

QY      5  TGACTGCATACAGCTTATATGACAGCATTTATAGCTCTCGCATATGTGAATTGCTAATA 64
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      216  TGAAGTGGTTAAACCTTTCATGCTGGATATAATACACAGCTGCATCATGATATATCCACCA 157

QY      65  CAGTTAAATAAACGTA 81
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      156  CCCTGTAAAAAATAGTA 140

RESULT 7
US-08-981-601-26/c
: Sequence 26, Application US/08981601
: Patent No. 6133023
: GENERAL INFORMATION:
: APPLICANT: MADSEN, Soeren Michael
: APPLICANT: VRANU, Astrid
: APPLICANT: ARNANU, Jose
: APPLICANT: RAVN, Peter
: APPLICANT: GROENVALD JOHNSSEN, Mads
: APPLICANT: ISRAELSEN, Hans
: TITLE OF INVENTION: A LACTIC ACID BACTERIAL REGULATABLE
: TITLE OF INVENTION: EXPRESSION SYSTEM

```

NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/981,601  
FILING DATE: 29-DEC-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/DK97/00341  
FILING DATE: 22-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/711,434  
FILING DATE: 06-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bent, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 030307/0158  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 170 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-981-601-26  
Query Match 26.8%; Score 27.6; DB 3; Length 170;  
Best Local Similarity 67.2%; Pred. No. 2.6;  
Matches 39; Conservative 0; Mismatches 19; Indels 0; Caps 0;  
QY 33 TTAATGCTCCTCGATGTGCAATGCTATACGTTAAACGTTATTCCTCG 90  
DB 116 TGAAGAATATATGTGTAATTAATTCGAATATAGTCATTAATAATGTTTTTTTGG 59  
RESULT 8  
US-08-179-557-17/C  
Sequence 17, Application US/08179557  
Patent No. 5837509  
GENERAL INFORMATION:  
APPLICANT: ISRAELSEN, Hans  
APPLICANT: BECH HANSEN, Egon  
APPLICANT: MADSEN, Soeren Michael  
APPLICANT: JOHANSEN, Eric  
APPLICANT: NILSSON, Dan  
APPLICANT: VRANG, Astrid  
TITLE OF INVENTION: Recombinant Lactic Acid Bacterium  
TITLE OF INVENTION: Containing an Inserted Promoter and Method of Constructing  
TITLE OF INVENTION: Same  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W.  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/179,557  
FILING DATE: 07-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 1579/92  
FILING DATE: 30-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 0988/93  
FILING DATE: 01-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK94/00004  
FILING DATE: 03-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/036,681  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30307/140/PLVI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202 672 5300  
TELEFAX: 202 672 5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1070 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-179-557-17  
Query Match 26.8%; Score 27.6; DB 2; Length 1070;  
Best Local Similarity 67.2%; Pred. No. 4;  
Matches 39; Conservative 0; Mismatches 19; Indels 0; Caps 0;

QY 33 TTAATGCTCCTCGATGTGCAATGCTATACGTTAAACGTTATTCCTCG 90  
DB 1016 TGAAGAATATATGTGTAATTAATTCGAATATAGTCATTAATAATGTTTTTTTGG 959  
RESULT 9  
US-08-200-900A-1  
Sequence 1, Application US/08200900A  
Patent No. 5665566  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc. - Legal Affairs  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: MA  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/200,900A  
FILING DATE: 23-FEB-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meiner, Maureen C.  
REGISTRATION NUMBER: 31,544  
REFERENCE/DOCKET NUMBER: GI 5201-FWC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 876-1170 X8574  
TELEFAX: (617) 876-5851

```

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 2581 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   US-08-200-900A-1

Query Match
Best Local Similarity 55.1%; Score 27.6; DB 1; Length 2581;
Matches 54; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 3 ACTGACTGGAATTAACAGTTTAATGACAGCATTAATAGCTCTGCAATATGTAATGCTAA 62
Db 2469 AGTTAAAAAAATAATTAATTAATAAAGTCTGATCTTACCTAAGGCACTGAAATGCTAC 2528
QY 63 TACAGTTAAAAAAGCGTATTTCCCTGCTTGATCA 100
Db 2529 AAAAAAACCAGGATTCAGCTTGACCTTAACCA 2566

RESULT 10
PCT-US94-00616-1
; Sequence 1, Application PC/TUS9400616
; GENERAL INFORMATION:
;   APPLICANT:
;   TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE
;   NUMBER OF SEQUENCES: 33
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   OPERATING SYSTEM: IBM PC compatible
;   SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US94/00616
;   FILING DATE:
;   CLASSIFICATION:
;   INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 2581 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;     PCT-US94-00616-1

Query Match
Best Local Similarity 55.1%; Score 27.6; DB 5; Length 2581;
Matches 54; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 3 AGTACTGGAATTAACAGTTTAATGACAGCATTAATAGCTCTGCAATATGTAATGCTAA 62
Db 2469 AGTTAAAAAAATAATTAATTAATAAAGTCTGATCTTACCTAAGGCACTGAAATGCTAC 2528
QY 63 TACAGTTAAAAAAGCGTATTTCCCTGCTTGATCA 100
Db 2529 AAAAAAACCAGGATTCAGCTTGACCTTAACCA 2566

RESULT 11
US-09-484-970B-138
; Sequence 138, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
;   APPLICANT: Jones, Karen A.
;   APPLICANT: Volkmut, Wayne
;   APPLICANT: Walker, Michael G.
;   TITLE OF INVENTION: BONE REMODELING GENES
;   FILE REFERENCE: PB-0014 US
;   CURRENT APPLICATION NUMBER: US/09/484, 970B
;   CURRENT FILING DATE: 2000-01-18
;   NUMBER OF SEQ ID NOS: 172
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```

; SOFTWARE: PERL Program
; SEQ ID NO 138
; LENGTH: 3054
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID NO. 6426186 336987.1CBI
;   US-09-484-970B-138

Query Match
Best Local Similarity 56.7%; Score 27.6; DB 4; Length 3054;
Matches 51; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 13 ATACAGTTTAATGACAGCATTAATAGCTCTGCAATATGTAATGCTTAACAGTTAA 72
Db 2256 ATAGAGAGCTTACTATATATATTAATTAAGTGCATATATTTACTTCAATACCTATATT 2315
QY 73 AAAACGGTATTTCCCTGCTTGATCA 102
Db 2316 AGAAGATATGTATGCTGACTGAATATATAC 2345

RESULT 12
US-09-539-333D-196
; Sequence 196, Application US/09539333D
; Patent No. 6476208
; GENERAL INFORMATION:
;   APPLICANT: Cohen, Daniel
;   APPLICANT: Blumenfeld, Marta
;   APPLICANT: Chumakov, Ilya
;   APPLICANT: Bougueleret, Lydie
;   APPLICANT: Bihain, Bernard
;   APPLICANT: Essiloux, Laurent
;   TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;   FILE REFERENCE: GENSET 047AUS
;   CURRENT APPLICATION NUMBER: US/09/539, 333D
;   CURRENT FILING DATE: 2000-03-30
;   PRIOR APPLICATION NUMBER: US 60/126, 903
;   PRIOR FILING DATE: 1999-03-30
;   PRIOR APPLICATION NUMBER: US 60/131, 971
;   PRIOR FILING DATE: 1999-04-30
;   PRIOR APPLICATION NUMBER: US 60/132, 065
;   PRIOR FILING DATE: 1999-04-30
;   PRIOR APPLICATION NUMBER: US 60/143, 928
;   PRIOR FILING DATE: 1999-07-14
;   PRIOR APPLICATION NUMBER: US 60/145, 915
;   PRIOR FILING DATE: 1999-07-27
;   PRIOR APPLICATION NUMBER: US 60/146, 453
;   PRIOR FILING DATE: 1999-07-29
;   PRIOR APPLICATION NUMBER: US 60/146, 452
;   PRIOR FILING DATE: 1999-07-29
;   PRIOR APPLICATION NUMBER: US 60/162, 288
;   PRIOR FILING DATE: 1999-10-28
;   PRIOR APPLICATION NUMBER: US 09/416, 384
;   PRIOR FILING DATE: 1999-10-12
;   NUMBER OF SEQ ID NOS: 231
;   SOFTWARE: Patent.pm
;   SEQ ID NO 196
;   LENGTH: 3001
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;     NAME/KEY: allele
;     LOCATION: 1501
;   OTHER INFORMATION: 99-26228-172 : polymorphic base G or C
;   NAME/KEY: misc_binding
;     LOCATION: 1482..1500
;   OTHER INFORMATION: 99-26228-172.m1s1
;   NAME/KEY: misc_binding
;     LOCATION: 1502..1521
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```

OTHER INFORMATION: 99-26228-172.mis2, complement
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1330..1350
OTHER INFORMATION: upstream amplification primer
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1792..1812
OTHER INFORMATION: downstream amplification primer, complement
FEATURE:
NAME/KEY: misc_binding
LOCATION: 1489..1513
OTHER INFORMATION: 99-26228-172 probe
US-09-539-333D-196

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Query Match	26.68;	Score 27.4;	DB 4;	Length 3001;
Best Local Similarity	55.98;	Pred. No. 6;		
Matches 52; Conservative	0;	Mismatches 41;	Indels 0;	Gaps 0;

Oy 3 AGTACTGGATAACAGTTTATGACAGCATTAACTCCTCATANGTAATGGCTAA 62  
 | |||| | | |||| | | | | |||| |  
 Db 418 AATACATGACGAGCATTACTGTCACAAAATATAAATAGAGTTATAGTAATTTGATAT 477

Qy 63 TACAGTAAAAAACGCTATTTCCTGGTCTG 95  
          || |||| | |||| | ||||  
Db 478 CCAGTAAAAAACAGCTATTTCCTCAATCTG 510

RESULT 13  
US-09-220-132-2  
; Sequence 2, Application US/09220132

```

? PATENT NO.: 6506607
? GENERAL INFORMATION:
? APPLICANT: Shyjan, Andrew W.
? TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
? TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
? FILE REFERENCE: 07334-074001
? CURRENT APPLICATION NUMBER: US/09/220,132
? PRIOR FILING DATE: 1998-12-23
? PRIOR APPLICATION NUMBER: US 60/079,303
? PRIOR FILING DATE: 1998-03-25
? PRIOR APPLICATION NUMBER: US 60/068,821
? PRIOR FILING DATE: 1997-12-24
? NUMBER OF SEQ ID NOS: 191
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 2
? LENGTH: 3508
? TYPE: DNA
? ORGANISM: Homo sapiens
? IS-09-220-132-2

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Query Match	26.6%;	Score 27.4;	DB 4;	Length 5508;
Best Local Similarity	62.3%;	Pred. No. 6.9;		
Matches 43;	Conservative 0;	Mismatches 26;	Indels 0;	Gaps 0;

0y 26 GACAGCATTTAATAGCTCCTGCATAGTGAAATTGCTAATACAGTTAAAAACGGTATTTC 85  
||||| | |||| |||| | ||||| |||| | ||||| | ||||  
Db 557 GACAGCTGAAAAAGCTATTGCCACACTGAATTCTTAATATGCGAAAAAGCTCTTATTAA 616

Qy	86	CCTGGTCT	94
		11111	
Db	617	TTTGTTC	625

RESULT 14  
US-09-410-464-9  
; Sequence 9, Application US/09410464

```

: Patent NO. 3395892
:
: GENERAL INFORMATION:
:
: APPLICANT: Strauss et al.
:
: TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering time
:
: TITLE OF INVENTION: poplar and other plant species.
:
: FILE REFERENCE: 53375

```

```

? CURRENT APPLICATION NUMBER: US/09/410,464
?
? CURRENT FILING DATE: 1999-10-01
? EARLIER APPLICATION NUMBER: 09/287,700
? EARLIER FILING DATE: 1999-04-06
? EARLIER APPLICATION NUMBER: 60/080,851
? EARLIER FILING DATE: 1998-04-06
?
? NUMBER OF SEQ ID NOS: 24
? SOFTWARE: PatentIn Ver. 2.0
?
? SEQ ID NO 9
?
? LENGTH: 11485
? TYPE: DNA
? ORGANISM: Populus balsamifera subsp. trichocarpa
? US-09-410-464-9

```

Query Match	26.68;	Score 27.4;	DB 4;	Length 11485;
Best Local Similarity	57.68;	Pred. NO. 8.3;		
Matches 49;	Conservative 0;	Mismatches 36;	Indels 0;	Gaps 0;

Oy	13 ATAAACGTTTAATGACAGACATTATPAGCCTGCATATGGAATGGCTATACGTAA 72
Ddb	6634 ATAAACCAATTAAAAAATCATTAATTATTATTTTTTAAATTAATAAAAACACTTA 66333

Qy	73	AAACGGTATTCCCTGGTCTGAT	97
Db	6694	AACACAGTATTACCCAATACAGAT	6718

RESULT 15  
US-09-734-674-3/c  
; Sequence 3, Application US/09734674  
Patent No. 640003

```

? PATENT NO.: 083602Z
? GENERAL INFORMATION:
?
? APPLICANT: WEI, Ming-Hui et al.
? TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
? TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
? TITLE OF INVENTION: AND USES THEREOF
? FILE REFERENCE: CLO01018
? CURRENT APPLICATION NUMBER: US/09/734,674
? CURRENT FILING DATE: 2000-12-13
? NUMBER OF SEQ ID NOS: 4
? SOFTWARE: FASTSEQ for Windows Version 4.0
?
? SEQ ID NO 3
? LENGTH: 202001
?
? TYPE: DNA
?
? ORGANISM: Human
?
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1)...(202001)
? OTHER INFORMATION: n = A,T,C OR G
?
? US-09-734-674-3

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Query Match	26.68;	Score 27.4;	DB 4;	Length 202001;
Best Local Similarity	62.38;	Pred. No. 17;		
Matches 43;	Conservative 0;	Mismatches 26;	Indels 0;	Gaps 0;

**QY** 5 TGACTGGAAATACAGTTAATGACAGCATTATAGTCCTGCATATGTGAATTGCTAATA 64  
| | | | |  
**Db** 93512 TCATTAGGATAACTTTCGTGAGGAAAGCATTTACAATAATTAAGAATGTCACAGA 93453

QY	65	CAGTTAAA	73
Db	93452	CTGGTAAA	93444

RESULT 16  
US-09-328-352-1715/c  
; Sequence 1715, Application US/09328352

```

; Patent No. 6562958
;
; GENERAL INFORMATION:
;
; APPLICANT: Gary L. Breton et al.
;
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
;
; TITLE OF INVENTION: BALMANNII FOR DIAGNOSTICS AND THERAPEUTICS
;
; FILE REFERENCE: GTC99-03PA

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;; CURRENT APPLICATION NUMBER: US/09/328,352  
;; CURRENT FILING DATE: 1999-06-04  
;; NUMBER OF SEQ ID NOS: 8252  
;; SEQ ID NO 1715  
;; LENGTH: 306  
;; TYPE: DNA  
;; ORGANISM: Acinetobacter baumannii  
US-09-328-352-1715

Query Match 26.4%; Score 27.2; DB 4; Length 306;  
Best Local Similarity 55.2%; Pred. No. 4;  
Matches 53; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 8 CTGGATTACAGTTTAATGACAGCATTAATAGCTCCTGATATGTAAATGCTAAACAG 67  
DB 212 CTAACTTAACAGACTGCACAGCATTAATTTCTTCTGATTTGCTAACTTCTGCTGG 153  
QY 68 TTAATAAAGGATTTCCCTGCTGATCCACA 103  
DB 152 CTTAAACGACGGCCTAAACCTGTTCTGATGCACA 117

RESULT 17  
US-09-601-198-108  
; Sequence 108, Application US/09601198  
; Patent No. 6531583

## GENERAL INFORMATION:

;; APPLICANT: Cassell, Gail H.  
;; APPLICANT: Chen, Ellison Y.  
;; APPLICANT: Glass, Jennifer S.  
;; APPLICANT: Glass, John I.  
;; APPLICANT: Helner, Cheryl R.  
;; APPLICANT: Lefkowitz, Elliot  
;; TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA  
;; TITLE OF INVENTION: UREALYTICUM  
;; FILE REFERENCE: UAB-13452/22  
;; CURRENT APPLICATION NUMBER: US/09/601,198  
;; CURRENT FILING DATE: 2000-12-08  
;; PRIOR APPLICATION NUMBER: 60/073,189  
;; NUMBER OF SEQ ID NOS: 181  
;; SOFTWARE: Patent In Ver. 2.0  
;; SEQ ID NO 108  
;; LENGTH: 3255  
;; TYPE: DNA  
;; ORGANISM: Ureaplasma urealyticum  
US-09-601-198-108

Query Match 26.4%; Score 27.2; DB 4; Length 3255;  
Best Local Similarity 64.1%; Pred. No. 7.1;  
Matches 41; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 20 TTTAATGACAGCATTAATAGCTCCTGATATGTGAATGCTAATCAAGTTAAACCG 79  
DB 520 TTTTCTTAATCAATTAAGCAGGTAATTTCTAATGACATATTTTGAACAAAGG 579  
QY 80 TATT 83  
DB 580 TTTT 583

RESULT 18  
US-08-930-996A-1/C  
; Sequence 1, Application US/08930996A  
; Patent No. 6100449

## GENERAL INFORMATION:

;; APPLICANT: FUJHR, Robert  
;; APPLICANT: ESHED, Yuval  
;; APPLICANT: ORI, Naomi  
;; APPLICANT: PARAN, Ilan  
;; APPLICANT: ZAMIR, Daniel  
;; TITLE OF INVENTION: A GENE FAMILY FROM THE I2 FUSARIUM RESISTANCE  
;; TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND

;; TITLE OF INVENTION: SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS  
;; NUMBER OF SEQUENCES: 12  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: BROWDY AND NEIMARK  
;; STREET: 419 Seventh Street, N.W., Suite 300  
;; City: Washington  
;; STATE: D.C.  
;; COUNTRY: USA  
;; ZIP: 20004

## COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: Patent In Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/930,996A

;; FILING DATE: 09-DEC-1997

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: PCT/US96/05272

;; FILING DATE: 15-APR-1996

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: IL 113,373

;; FILING DATE: 13-APR-1995

;; INFORMATION FOR SEQ. ID NO: 1:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 4946 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: cDNA

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: 299..3958

US-08-930-996A-1

Query Match 26.4%; Score 27.2; DB 3; Length 4946;  
Best Local Similarity 56.8%; Pred. No. 7.9;  
Matches 50; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 8 CTGGATAAAGCTTAATGACAGCATTAATAGCTCCTGATATGTGAATGCTAATACAG 67  
DB 2802 CTGCATAGACCTCTCTGACACACTTATCCATGCATCCCTAATGAAAGGAT 2743  
QY 68 TTAATAAAGGATTTCCCTGCTGCTG 95  
DB 2742 TCCAAACAGGAGGTCTCTAGTGTG 2715

## RESULT 19

US-09-328-352-1417  
; Sequence 1417, Application US/09328352  
; Patent No. 6562958

## GENERAL INFORMATION:

;; APPLICANT: Gary L. Breton et al.  
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
;; FILE REFERENCE: GTC99-03PA  
;; CURRENT APPLICATION NUMBER: US/09/328,352  
;; CURRENT FILING DATE: 1999-06-04  
;; NUMBER OF SEQ ID NOS: 8252  
;; SEQ ID NO 1417  
;; LENGTH: 1287  
;; TYPE: DNA  
;; ORGANISM: Acinetobacter baumannii  
US-09-328-352-1417

Query Match 26.2%; Score 27; DB 4; Length 1287;  
Best Local Similarity 60.0%; Pred. No. 6.6;  
Matches 45; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 19 GTTAAATGACAGCATTAATAGCTCCTGATATGTGAATGCTAATCAAGTTAAACCG 78  
DB 548 GTTAAATGACAGCATTTTAGTTCCTTTCTTATTTTGTAGACGTAATGTGACT 607



Query Match	26.0%;	Score 26.8;	DB 4;	Length 1830121;
Best Local Similarity	64.5%;	Pred. No. 40;		
Matches 40;	Conservative 0;	Mismatches 22;	Indels 0;	Gaps 0;



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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,409
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/680,726
FILING DATE: 12-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-46-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1038 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1035
US-09-092-409-53
```

```
Query Match 25.8%; Score 26.6; DB 3; Length 1038;
Best Local Similarity 60.3%; Pred. No. 8.4;
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
```

```
QY 13 ATAAAGTTTAATGACGATTAATAGCTCTGCATATGCAATTGCTAATACAGTTAA 72
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 640 AAAAAGTTCATGCTCACTTTGATGCTCTACAGATCTAGATTCTTACACATTCCA 581
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QY 73 AAACGGTATTTC 85
| | | | | | | | | |
DB 580 TAAAGTTGGTTC 568
```

```
RESULT 26
US-08-220-151-18/C
Sequence 18, Application US/08220151
Patent No. 5529780
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Limbach, Keith J.
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
TITLE OF INVENTION: CANINE HERPESVIRUS gB, gC AND gD AND USES THEREFOR
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,151
FILING DATE: 30-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
```

```
REFERENCE/DOCKET NUMBER: 454310-2540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-220-151-18
```

```
Query Match 25.8%; Score 26.6; DB 1; Length 1320;
Best Local Similarity 60.3%; Pred. No. 8.9;
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
```

```
QY 13 ATAAAGTTTAATGACGATTAATAGCTCTGCATATGCAATTGCTAATACAGTTAA 72
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 840 AAAAAGTTCATGCTCACTTTGATGCTCTACAGATCTAGATTCTTACACATTCCA 781
```

```
QY 73 AAACGGTATTTC 85
| | | | | | | | | |
DB 780 TAAAGTTGGTTC 768
```

```
RESULT 27
US-08-413-118-18/C
Sequence 18, Application US/08413118
Patent No. 5688920
GENERAL INFORMATION:
APPLICANT: PAOLETTI, ENZO
APPLICANT: LIMBACH, KEITH J.
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
TITLE OF INVENTION: CANINE HERPESVIRUS gB, gC, AND gD AND USES THEREFOR
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
STREET: 530 FIFTH AVENUE, 25TH FLOOR
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: UNITED STATES OF AMERICA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,118
FILING DATE: 29-MAR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,151
FILING DATE: 30-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2670
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-413-118-18
```

```
Query Match 25.8%; Score 26.6; DB 1; Length 1320;
```



MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/473,446  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/413,118  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FROMMER, WILLIAM S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2670  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 126:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1415 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-473-446-126

Query Match 25.8%; Score 26.6; DB 3; Length 1415;  
Best Local Similarity 60.3%; Pred. No. 9.1;  
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 13 ATAAAGTTTAATGACGATTAATAGCTCCCTGCATATGCGATTGCTAATACAGTTAA 72  
DB 939 AAAAAGTTCACTGCTACACTTTGATGCTCTACAGATCTAGATCTTACACCATTC 880  
QY 73 AAACGGTATTTC 85  
DB 879 TAAAGTTGGTTC 867

RESULT 31  
US-08-680-726A-51/C  
Sequence 51, Application US/08680726A  
Patent No. 5804197  
GENERAL INFORMATION:  
APPLICANT: Haanes, Elizabeth J.  
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES  
NUMBER OF SEQUENCES: 92  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, Suite 3500  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.A.  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/680,726A  
FILING DATE: 12-JUL-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-46-C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:  
LENGTH: 10592 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-680-726A-51

Query Match 25.8%; Score 26.6; DB 1; Length 10592;  
Best Local Similarity 60.3%; Pred. No. 15;  
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 13 ATAAAGTTTAATGACGATTAATAGCTCCCTGCATATGCGATTGCTAATACAGTTAA 72  
DB 5767 AAAAAGTTCACTGCTACACTTTGATGCTCTACAGATCTAGATCTTACACCATTC 5708  
QY 73 AAACGGTATTTC 85  
DB 5707 TAAAGTTGGTTC 5695

RESULT 32  
US-08-680-726A-52  
Sequence 52, Application US/08680726A  
Patent No. 5804197  
GENERAL INFORMATION:  
APPLICANT: Haanes, Elizabeth J.  
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES  
NUMBER OF SEQUENCES: 92  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, Suite 3500  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.A.  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/680,726A  
FILING DATE: 12-JUL-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-46-C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10592 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-680-726A-52

Query Match 25.8%; Score 26.6; DB 1; Length 10592;  
Best Local Similarity 60.3%; Pred. No. 15;  
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 13 ATAAAGTTTAATGACGATTAATAGCTCCCTGCATATGCGATTGCTAATACAGTTAA 72  
DB 4826 AAAAAGTTCACTGCTACACTTTGATGCTCTACAGATCTAGATCTTACACCATTC 4885  
QY 73 AAACGGTATTTC 85  
DB 4886 TAAAGTTGGTTC 4898

```
RESULT 33
US-09-092-409-51/c
Sequence 51, Application US/09092409
Patent No. 6159478
GENERAL INFORMATION:
APPLICANT: Haanes, Elizabeth J.
APPLICANT: Frank, Rexann S.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,409
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/680,726
FILING DATE: 12-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-46-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 10592 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-092-409-51

Query Match      25.8%; Score 26.6; DB 3; Length 10592;
Best Local Similarity 60.3%; Pred. No. 15;
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 13 ATACAGTTTAATGACAGCATTATAGCTCGCATATGTAATTGCTAATACAGTTAAA 72
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 5767 AAAAAGTTTCATCGTCACATTGATGCTCTACAGATCTAGATTCCTTACACCAATCCA 5708
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 73 AAACGGTATTTTC 85
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 5707 TAAAGTTGCTTC 5695
```

```
RESULT 34
US-09-092-409-52
Sequence 52, Application US/09092409
Patent No. 6159478
GENERAL INFORMATION:
APPLICANT: Haanes, Elizabeth J.
APPLICANT: Frank, Rexann S.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado

Query Match      25.8%; Score 26.6; DB 3; Length 10592;
Best Local Similarity 60.3%; Pred. No. 15;
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 13 ATACAGTTTAATGACAGCATTATAGCTCGCATATGTAATTGCTAATACAGTTAAA 72
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 4826 AAAAAGTTTCATCGTCACATTGATGCTCTACAGATCTAGATTCCTTACACCAATCCA 4885
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 73 AAACGGTATTTTC 85
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 4886 TAAAGTTGCTTC 4898

RESULT 35
US-09-702-705-655/c
Sequence 655, Application US/09702705
Patent No. 6504010
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodges, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedrick, Tom
APPLICANT: Carter, Darriek
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 655
LENGTH: 494
TYPE: DNA
ORGANISM: Homo sapien
US-09-702-705-655

Query Match      25.6%; Score 26.4; DB 4; Length 494;
Best Local Similarity 65.0%; Pred. No. 8.2;
Matches 39; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
```



APPLICANT: Baker, Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C13  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088026  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088028  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088326  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167

PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088212  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088217  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088655  
PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088738  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088742  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088810  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089440  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
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Best Local Similarity 57.18; Pred. No. 11;
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; Sequence 17, Application US/08616368A
; Patent No. 5767262
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; APPLICANT: Haber, Edgar
; APPLICANT: Jain, Mukesh
; APPLICANT: Yet, Shaw-Fang
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; TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/616,368A
; FILING DATE: 15-MAR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/022001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8306
; TELEX: 200154
; INFORMATION FOR SEQ. ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-616-368a-17
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; APPLICANT: Lee, Mu-En
; APPLICANT: Haber, Edgar
; APPLICANT: Jain, Mukesh
; APPLICANT: Yet, Shaw-Fang
; TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
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; OPERATING SYSTEM: Windows 95
; SOFTWARE: FASTSEQ for Windows Version 2.0b
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; APPLICATION NUMBER: US/09/054,298
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; SEQUENCE CHARACTERISTICS:

APPLICANT: Kijavira, Ivar J.

APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC13  
CURRENT APPLICATION NUMBER: US/09/996,243  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
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; PRIOR FILING DATE: 1998-07-09

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; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurneidi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C13
; CURRENT APPLICATION NUMBER: US/09/996,243
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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#### SUMMARIES

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C 4	30.4	29.5	702	US-10-027-632-202237	Sequence 202237,
C 5	29.8	28.9	177556	US-09-952-213b-6	Sequence 6, Appl1
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C 7	29.4	28.5	31412	US-10-109-551-3	Sequence 3, Appl1
C 8	29.2	28.3	585	US-10-027-632-320680	Sequence 320680,
C 9	29.2	28.3	1270	US-10-027-632-79603	Sequence 79603, A
C 10	29.2	28.3	148567	US-09-801-8768-3	Sequence 3, Appl1
C 11	29.2	28.3	148567	US-10-254-869-3	Sequence 3, Appl1
C 12	29	28.2	687	US-10-027-632-11949	Sequence 11949, A
C 13	28.8	28.0	1830121	US-10-329-960-1	Sequence 1, Appl1
C 14	28.4	27.6	2692	US-10-114-170-215	Sequence 106, App
C 15	28	27.2	466	US-09-989-722-106	Sequence 106, App
C 16	28	27.2	466	US-09-989-723-106	Sequence 106, App

C 17	28	27.2	466	9	US-09-989-279-106	Sequence 106, App
C 18	28	27.2	466	9	US-09-989-727-106	Sequence 106, App
C 19	28	27.2	466	10	US-09-989-731-106	Sequence 106, App
C 20	28	27.2	466	10	US-09-989-732-106	Sequence 106, App
C 21	28	27.2	466	10	US-09-991-073-106	Sequence 106, App
C 22	28	27.2	466	10	US-09-990-442-106	Sequence 106, App
C 23	28	27.2	466	10	US-09-991-163-106	Sequence 106, App
C 24	28	27.2	466	10	US-09-993-604-106	Sequence 106, App
C 25	28	27.2	466	10	US-09-980-456-106	Sequence 106, App
C 26	28	27.2	466	10	US-09-989-721-106	Sequence 106, App
C 27	28	27.2	466	10	US-09-982-598-106	Sequence 106, App
C 28	28	27.2	466	10	US-09-989-293A-106	Sequence 106, App
C 29	28	27.2	466	10	US-09-989-735-106	Sequence 106, App
C 30	28	27.2	466	10	US-09-981-144-106	Sequence 106, App
C 31	28	27.2	466	10	US-09-989-730-106	Sequence 106, App
C 32	28	27.2	466	10	US-09-990-436-106	Sequence 106, App
C 33	28	27.2	466	10	US-09-993-687-106	Sequence 106, App
C 34	28	27.2	466	11	US-09-989-734-106	Sequence 106, App
C 35	28	27.2	466	11	US-09-997-653-106	Sequence 106, App
C 36	28	27.2	466	11	US-09-983-667-106	Sequence 106, App
C 37	28	27.2	466	11	US-09-987-428-106	Sequence 106, App
C 38	28	27.2	466	11	US-09-997-666-106	Sequence 106, App
C 39	28	27.2	466	11	US-09-990-438-106	Sequence 106, App
C 40	28	27.2	466	11	US-09-990-562-106	Sequence 106, App
C 41	28	27.2	466	11	US-09-980-711-106	Sequence 106, App
C 42	28	27.2	466	11	US-09-989-726-106	Sequence 106, App
C 43	28	27.2	466	11	US-09-989-156-106	Sequence 106, App
C 44	28	27.2	466	11	US-09-998-437-106	Sequence 106, App
C 45	28	27.2	466	11	US-09-990-437-106	Sequence 106, App

#### ALIGNMENTS

RESULT 1  
US-10-274-974-3/C  
Sequence 3, Application US/10274974  
Publication No. US20030054490A1  
GENERAL INFORMATION:  
APPLICANT: WEI, Ming-Hui et al.  
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,  
TITLE OF INVENTION: AND USE THEREOF  
FILE REFERENCE: CLO00871 DIV  
CURRENT APPLICATION NUMBER: US/10/274,974  
CURRENT FILING DATE: 2002-10-18  
PRIOR APPLICATION NUMBER: 09/685,853  
PRIOR FILING DATE: 2000-10-11  
PRIOR APPLICATION NUMBER: 60/182,194  
PRIOR FILING DATE: 2000-02-14  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 74962  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: (1)...(74962)  
OTHER INFORMATION: n = A,T,C or G  
US-10-274-974-3

Query Match 35.1%; Score 36.2; DB 14; Length 74962;  
Best Local Similarity 62.9%; Pred. No. 0.89;  
Matches 56; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 12 AATAACATTTAATGACGACATTTACTCTGATATGTAATTCGTAATACAGTTAA 71  
DB 63338 AAAAAAAAAAATTCACGATTCACAAACCCCTAGACGACTTACTTCAATCAATTA 63279  
QY 72 AAAAAAGGATTTCCCTGCTCTGATCA 100  
DB 63278 AAAAAAGGCTTTTCAGTACTTCTCATCTA 63250

```
RESULT 2
US-10-027-632-230735/c
; Sequence 230735, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 230735
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-230735

Query Match
Best Local Similarity 31.1%; Score 32; DB 13; Length 585;
Matches 56; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 2 AAGTACTGGAATACAGATTATGACACCATTAAGTCTCGATATGTAATGCTTA 61
DB 318 AATGATGATTCCTTCATTTATTAACAAGGATTAAGCCCATATTAATGTTCTTACAA 259
QY 62 ATACAGTTAAAAAGCGATTTCCCTGGTCTGAT 97
DB 258 CAGAGGTCTATTATGTTTCCATCTTACTGAT 223

RESULT 3
US-10-027-632-202236/c
; Sequence 202236, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 202236
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-202236

Query Match
Best Local Similarity 29.5%; Score 30.4; DB 13; Length 702;
Matches 49; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 11 GAATAACGTTTAATGACATTAATAGCTCTGATATGTAATGCTTAATACAGTTA 70
DB 667 GGAGTACATTTTATGATCTTTTATGTTGTAATAGAGATTGTAATAATACATTTA 608
QY 71 AAAAAACGTTATTCCTGG 90
DB 607 AAAAAAATGTTCCCTAG 588

RESULT 4
US-10-027-632-202237/c
; Sequence 202237, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202237
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-202237

Query Match
Best Local Similarity 29.5%; Score 30.4; DB 13; Length 702;
Matches 49; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 11 GAATAACGTTTAATGACATTAATAGCTCTGATATGTAATGCTTAATACAGTTA 70
DB 667 GGAGTACATTTTATGATCTTTTATGTTGTAATAGAGATTGTAATAATACATTTA 608
QY 71 AAAAAACGTTATTCCTGG 90
DB 607 AAAAAAATGTTCCCTAG 588

RESULT 5
US-09-952-213D-6/c
; Sequence 6, Application US/09952213D
; Publication No. US20030096240A1
; GENERAL INFORMATION:
; APPLICANT: MURAD, FERID
; APPLICANT: SHARINA, IRAIDA G.
; APPLICANT: KRUMENACKER, J. S.
; APPLICANT: MARTIN, E.
```



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; TITLE OF INVENTION: GENOMIC ORGANIZATION OF MOUSE AND HUMAN SGC
; FILE REFERENCE: UTSR:252US
; CURRENT APPLICATION NUMBER: US/09/952.213D
; CURRENT FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 177556
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (2293..144567)
; OTHER INFORMATION: N = A, C, T/U OR G
US-09-952-213D-6

Query Match      28.9%; Score 29.8; DB 11; Length 177556;
Best Local Similarity 56.7%; Pred. No. 1.1e+02;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

OY      2  AACTGACTGGAATTAACAGTTTAATGACAGCATTAATGCTCCGATATGTGAATTCCTA 61
Db      96352  AAGAGCATGAACATTAATTCATGACAGATCCATCGAATTCACAAATTCAGATGATC 96293

OY      62  ATACAGTTAAATAAACGGTATTTCCCTGGTTCGATC 98
Db      96292  AAAAATTAAAGAAATATCTTTTCTCTATCTTATC 96256

RESULT 6
US-10-027-632-245609
; Sequence 245609, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 245609
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-245609

Query Match      28.7%; Score 29.6; DB 13; Length 533;
Best Local Similarity 57.6%; Pred. No. 18;
Matches 53; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

OY      2  AACTGACTGGAATTAACAGTTTAATGACAGCATTAATGCTCCGATATGTGAATTCCTA 61
Db      353  AAATAGCTGGATTTACAGGTGTGGCCACCATGCTGCTATGTGTGTGTGTTTA 412

OY      62  ATACAGTTAAATAAACGGTATTTCCCTGGTTC 93
Db      413  TTTTGTAGAGATAGAGGTTTTGCATGTTTC 444
```

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RESULT 7
US-10-109-551-3/C
; Sequence 3, Application US/10109551
; Publication No. US20020194635A1
; GENERAL INFORMATION:
; APPLICANT: DUNNE, PATRICK W.
; APPLICANT: PIEDRAHITA, JORGE
; TITLE OF INVENTION: TRANSGENIC ANIMALS RESISTANT TO TRANSMISSIBLE
; FILE REFERENCE: TAMK:20705
; CURRENT APPLICATION NUMBER: US/10/109.551
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/280,549
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 31412
; TYPE: DNA
; ORGANISM: Ovis aries
US-10-109-551-3

Query Match      28.5%; Score 29.4; DB 13; Length 31412;
Best Local Similarity 63.4%; Pred. No. 81;
Matches 45; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

OY      13  ATACAGTTTAATGACAGCATTAATGCTCCGATATGTGAATTCGTAATGCTTAATACAGTTAA 72
Db      21603  ATATCTGTTAAAGAGANTTAACATCTTCTGAAACATATTAATGACACAGAAATTTTA 21544

OY      73  AAAACGGTATT 83
Db      21543  TCAAGGAATT 21533

RESULT 8
US-10-027-632-320680/C
; Sequence 320680, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 320680
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-320680

Query Match      28.3%; Score 29.2; DB 13; Length 585;
Best Local Similarity 62.2%; Pred. No. 25;
Matches 46; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

OY      30  GCATTAACTCCTGCTGATATGTAATTCGCTAATACAGTTAAATAAACGGTATTTCCCTG 89
```

Db 384 GCATTATACAGCTTCCAAATCTTAATGATTTGACTGTGACACACAGGACTTCCAAAG 325  
QY 90 GTTCGTATCCACA 103  
Db 324 GGTGTCAATCAACA 311

## RESULT 9

US-10-027-632-79603/c  
; Sequence 79603, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1998-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 79603  
; LENGTH: 1270  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-79603

Query Match 28.3%; Score 29.2; DB 13; Length 1270;  
Best Local Similarity 62.2%; Pred. No. 32;  
Matches 46; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
QY 30 GCATTATAGCTCTGCATATGTGATTCCTTAATACAGTTAAAAACGGTATTTCCCTG 89  
Db 1063 GCATTATACAGCTTCCAAATCTTAATGATTTGACTGTGACACACAGGACTTCCAAAG 1004  
QY 90 GTTCGTATCCACA 103  
Db 1003 GGTGTCAATCAACA 990

## RESULT 10

US-09-801-876B-3/c  
; Sequence 3, Application US/09801876B  
; Patent No. US20020127683A1  
; GENERAL INFORMATION:  
; APPLICANT: Ye, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEROF  
; FILE REFERENCE: C1001160  
; CURRENT APPLICATION NUMBER: US/09/801,876B  
; CURRENT FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 148567  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature

; LOCATION: (1)...(148567)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-801-876B-3

Query Match 28.3%; Score 29.2; DB 10; Length 148567;  
Best Local Similarity 56.1%; Pred. No. 1.5e+02;  
Matches 55; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 5 TGACGTGAATTAACAGTTTAATGACAGCATTATAGCTCCGTGATGTGTAATGCTAATA 64  
Db 73685 TGCATTGCATTAATATGTAATACACATTAAATATTTCTTTTGGCTGTAATGCTCACT 73626

QY 65 CAGTTAAAAAACGGTATTTCCCTGTTCTGATCCAC 102  
Db 73625 AATTGAACAAAGAAATTTGTGCCCTGCTATTCTTAAC 73588

## RESULT 11

US-10-254-869-3/c  
; Sequence 3, Application US/10254869  
; Publication No. US20030027307A1  
; GENERAL INFORMATION:  
; APPLICANT: Ye, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: C1001160DIV  
; CURRENT APPLICATION NUMBER: US/10/254,869  
; CURRENT FILING DATE: 2002-09-26  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 148567  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(148567)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-254-869-3

Query Match 28.3%; Score 29.2; DB 14; Length 148567;  
Best Local Similarity 56.1%; Pred. No. 1.5e+02;  
Matches 55; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 5 TCACGTGAATTAACAGTTTAATGACAGCATTATAGCTCCGTGATGTGTAATGCTAATA 64  
Db 73685 TGCATTGCATTAATATGTAATACACATTAAATATTTCTTTTGGCTGTAATGCTCACT 73626

QY 65 CAGTTAAAAAACGGTATTTCCCTGTTCTGATCCAC 102  
Db 73625 AATTGAACAAAGAAATTTGTGCCCTGCTATTCTTAAC 73588

## RESULT 12

US-10-027-632-11949/c  
; Sequence 11949, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363

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: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 11949
: LENGTH: 687
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-11949

Query Match      28.2%; Score 29; DB 13; Length 687;
Best Local Similarity 62.0%; Pred. No. 30;
Matches 44; Conservative 1; Mismatches 26; Indels 0; Gaps 0;

QY      4 GTGACTGATATACGATTATATGACAGCATTATAGCTCCTGCATATGTAATGCTAAT 63
Db      410 GTGACTGACAAAGACAGACAGACACATTTAAGGCTTTTATGTGTATATAGAAAT 351
QY      64 ACAGTTAAAA 74
Db      350 ATTGTAATTA 340

RESULT 13
US-10-329-960-1/c
: Sequence 1, Application US/10329960
: Publication No. US20030099277A1
: GENERAL INFORMATION:
: APPLICANT: Fleischmann et al.
: TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Frag
: FILE REFERENCE: PB186P1
: CURRENT APPLICATION NUMBER: US/10/329,960
: PRIOR FILING DATE: 2003-01-02
: PRIOR APPLICATION NUMBER: US 09/643,990
: PRIOR FILING DATE: 2000-08-23
: PRIOR APPLICATION NUMBER: US 08/487,429
: PRIOR FILING DATE: 1995-06-07
: PRIOR APPLICATION NUMBER: US 08/426,787
: PRIOR FILING DATE: 1995-04-21
: NUMBER OF SEQ ID NOS: 1
: SOFTWARE: Patentin Version 3.1
: SEQ ID NO 1
: LENGTH: 1830121
: TYPE: DNA
: ORGANISM: Haemophilus influenzae
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (4747)..(4747)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (9921)..(9921)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (10150)..(10150)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (29298)..(29298)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (36543)..(36543)
: OTHER INFORMATION: n equals a, t, g or c
: NAME/KEY: misc_feature
: LOCATION: (36551)..(36551)
: OTHER INFORMATION: n equals a, t, g or c
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: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (36636)..(36636)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (40808)..(40810)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (44416)..(44416)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (44905)..(44905)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (44975)..(44975)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (45593)..(45593)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (45732)..(45732)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (47036)..(47036)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (51334)..(51334)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (51602)..(51602)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (51786)..(51786)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (51805)..(51805)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (55369)..(55369)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (65309)..(65309)
: OTHER INFORMATION: n equals a, t, g or c
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: LOCATION: (65313)..(65313)
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: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (80024)..(80024)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (100091)..(100091)
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: NAME/KEY: misc_feature
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: OTHER INFORMATION: n equals a, t, g or c
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; LOCATION: (152500) ..(152500)
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; NAME/KEY: misc.feature
; LOCATION: (152530) ..(152530)

Query Match      28.0%; Score 28.8; DB 14; Length 1830121;
Best Local Similarity   58.0%; Pred. NO. 3.9e+02;
Matches    51; Conservative    0; Mismatches    37; Indels     0; Gaps     0;

QY          13 ATACAGCTTATGACAGCATTAATAGCTCCGTGCATATGCAATTGGTAATAATACGTTAA 72
           ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB         1541231 ATTAAAGAGTGCTGTTATTTTCCTAATAGTAGTGCATGATGATATTATTTCCATTTTAA 154117Z
QY          73 AAAACGGATATTCTCCGTGCTCGATCCA 100
           |||| | | |||| | | | | | | | | | |
DB        1541171 AAAAATATATATTCCTCTATCTCATTCCA 1541144

RESULT 14
US-10-114-170-215/c
; Sequence 215, Application US/10114170
; Publication No. US20030023075A1
; GENERAL INFORMATION:
APPLICANT: Blatner, Frederick R.
          Burland, Valerie
          Perna, Nicole T.
          Plunkett, Guy
          Welch, Rod
TITLE OF INVENTION: NO. US20030023075A1el Sequences of E. coli O157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Quarles & Brady
STREET: I South Pluckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/114,170
FILING DATE: 01-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/453, 702
FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110, 955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296 .95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 2692
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
US-10-114-170-215
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Query Match      27.6%  Score 28.4;  DB 14;  Length 2692;
Best Local Similarity 54.9%  Pred. No. 72;
Matches 56;  Conservative 0;  Mismatches 46;  Indels 0;  Gaps 0;

QY      2  AAGTACTGGAATTAACGTTTAATGACAGCATTAATAGCTCCATATGTGAATGCTA 61
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Db      1129  ACGGATGCGACTATATTTTATTTGCGAAGAAATGAAGACTACGAAATGTTTCTT 1070

QY      62  ATACAGTTAAAAAAGCGTATTTCCGTTCTGATCCACACA 103
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1069  TTTTGACAAATATATAAACACTTATGGAAGATCGATTGACACA 1028

RESULT 15
US-09-989-722-106/c
; Sequence 106, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC63
; CURRENT APPLICATION NUMBER: US/09/989,722
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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Query Match 27.2%; Score 28; DB 9; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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Db 216 TGAGTGTGTTAATCTTTCATGCTGGATAAATACAGCTGCATCTATGTAATCCACCA 157  
QY 65 CAGTTAAAAACGGTA 81  
Db 156 CCCTGTAAAAAATAGTA 140

RESULT 17  
US-09-989-279-106/c  
Sequence 106, Application US/09989279  
Patent No. US20020072496A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2730PIC56  
CURRENT FILING DATE: 2001-11-19  
CURRENT APPLICATION NUMBER: US/09/989,279  
PRIOR FILING DATE: 1997-06-16  
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;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
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;; PRIOR APPLICATION NUMBER: 60/091519  
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;; PRIOR APPLICATION NUMBER: 60/091626  
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;; PRIOR APPLICATION NUMBER: 60/091633  
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;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 9; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 5 TGACGTGGAATACAGCTTTAATGACACAGCATTAATAGCTCCTGCATATGATGATTCGCTAATA 64  
DB 216 TGACGTGTTAATATCTTTCATGCTGATTAATAACAGCTGCATCTATGATTAATCCACCA 157  
OY 65 CAGTTAAAAAACGGTA 81

Db 156 CCCTGTAATAAATAGTA 140  
RESULT 18  
US-09-989-727-106/c  
; Sequence 106, Application US/09989727  
; Patent No. US20020072497A1  
; GENERAL INFORMATION:  
; APPLICANT: Asinkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gunney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC65  
; CURRENT APPLICATION NUMBER: US/09/989,727  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
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; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
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; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088026  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088028

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26	PRIOR FILING DATE: 1998-06-25
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31	PRIOR APPLICATION NUMBER: 60/090682
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36	PRIOR FILING DATE: 1998-06-26
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38	PRIOR FILING DATE: 1998-07-01
39	PRIOR APPLICATION NUMBER: 60/091478
40	PRIOR FILING DATE: 1998-07-02
41	PRIOR APPLICATION NUMBER: 60/091544
42	PRIOR FILING DATE: 1998-07-01
43	PRIOR APPLICATION NUMBER: 60/091519
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46	PRIOR FILING DATE: 1998-07-02
47	PRIOR APPLICATION NUMBER: 60/091633
48	PRIOR FILING DATE: 1998-07-02
49	PRIOR APPLICATION NUMBER: 60/091978
50	PRIOR FILING DATE: 1998-07-07
51	PRIOR APPLICATION NUMBER: 60/091982
52	PRIOR FILING DATE: 1998-07-07
53	PRIOR APPLICATION NUMBER: 60/092182
54	PRIOR FILING DATE: 1998-07-09

Query Match	27.2%	Score 28;	DB 9;	Length 466;
Best Local Similarity	59.7%;	Pred. No. 53;		
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OY	5	TGACTGGAATPACAGTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATA	64	
Db	216	TGAATGGTTNAAATCTTTTCATGTGGTAATAATAACACCTGCATCTATGATATATCCACCA	157	
OY	65	CAGTTAAAAAACGTA	81	
Db	156	CCCTGTAAAAAATAGTA	140	

RESULT 19  
US-09-989-731-106/c  
; Sequence 106, Application US/09989731  
; Patent No. US20020103125A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gertlisen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C70  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/049787  
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;; PRIOR FILING DATE: 1998-06-26  
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;; PRIOR FILING DATE: 1998-07-01  
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;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 10; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 5 TGACTGANTACAGTTTATGACAGCATTATAGCTTCGCATATGTAATGCTAATA 64  
DB 216 TGACTGCTTNAATCTTCATGCTGATATAATACAGCTGCATCTATGATAATGCCACCA 157

OY 65 CAGTTAAAAAAGCGTA 81  
DB 156 CCCTGTAAAAAATAGTA 140

RESULT 20  
US-09-989-732-106/c

;; Sequence 106, Application US/09989732  
;; Patent No. US20020123463A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerttsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kijavlin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730PIC57  
;; CURRENT FILING DATE: 2001-11-19  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
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PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
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PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 27.2% Score 28; DB 10; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 5 TGACGCAATTAAGTGAATGACAGCATTAATAGCTCTGCATATGTAATGCTAATA 64  
DB 216 TGAGTGGTTNAAATCTTTACATGCGGATTAATAACAGCTGATGATTAATCCACCA 157  
OY 65 CAGTTAAAAAAGGTA 81  
DB 156 CCGCTGTAATAAATAGTA 140

RESULT 21  
US-09-991-073-106/c  
; Sequence 106, Application US/09991073  
; Patent No. US20020127576A1  
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC15  
CURRENT APPLICATION NUMBER: US/09/991,073  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
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PRIOR FILING DATE: 1998-04-28  
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PRIOR FILING DATE: 1998-05-07  
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;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 10; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 5 TGACTGGAATACAGTTTAATGACAGCAATTAATGCTCCGCAATATGTGAATTCCTAATA 64  
DB 216 TGAGTGGTTNAAATCTTTCATGGTGGATAAATACAGCTGCATCATATGATTAATCCACCA 157  
OY 65 CAGTTAAAAAACCGTA 81  
DB 156 CCGTGTAAAAAATAGTA 140

RESULT 22  
US-09-990-442-106/c  
; Sequence 106, Application US/09990442  
; Patent No. US20020132252A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David

;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Grimaldi, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gunney, Austin L.  
;; APPLICANT: Kijavini, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730P1C8  
;; CURRENT APPLICATION NUMBER: US/09/990,442  
;; CURRENT FILING DATE: 2001-11-14  
;; PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR FILING DATE: 1998-06-24  
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PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
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PRIOR FILING DATE: 1998-06-24  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 10; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 5 TGACGTGGAATACACTTTAATGACAGCATTAATAGCTCTCGATATGCAATTCCTAATA 64  
DB 216 TGAGTGGTTNAATCTTCATGCTGGATTAATACAGCTGCATCTAATGATTAATCCACA 157  
OY 65 CAGTTAAAAAAGCGSTA 81  
DB 156 CCCTGTAAAAAATAGTA 140

RESULT 23  
US-09-991-163-106/c  
Sequence 106, Application US/09991163  
Patent No. US20020132253A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone



APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
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APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C17  
CURRENT APPLICATION NUMBER: US/09/991,163  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match          27.2%  Score 28; DB 10; Length 466;
Best Local Similarity 59.7%  Pred No 53;
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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Db      216 TGAGTGTTAAATCTTCAATGCTGGATAAATACAGCTGCTATGATATACACCA 157
OY      65 CAGTTAAAAAACGTA 81
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Db      156 CCGTGTAATAAATAAGTA 140
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RESULT 24
US-09-993-604-106/c
Sequence 106; Application US/0993604
Patent No. US20020137075A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
```

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APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC25
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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Patent No. US20020137890A1  
GENERAL INFORMATION:  
;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
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FILE REFERENCE: P2730PIC22  
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PRIOR FILING DATE: 1998-06-24  
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; APPLICANT: Baker, Kevin P.													
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; APPLICANT: Kijavini, Ivar J.													
; APPLICANT: Napier, Mary A.													

APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
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APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
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APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC55  
CURRENT APPLICATION NUMBER: US/09/989,721  
CURRENT FILING DATE: 2001-11-19  
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Query Match 27.2%; Score 28; DB 10; Length 466;  
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Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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QY 65 CAGTTAAAAAAGCGTA 81  
DB 156 CCGCTGTAATAAATAGTA 140

RESULT 27  
US-09-992-598-106/c  
Sequence 106, Application US/09992598  
Patent No. US20020160384A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, V. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C20  
CURRENT APPLICATION NUMBER: US/09/992,598  
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: PRIOR FILING DATE: 1998-07-09

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QY 65 CAGTTAAAAAACGCTA 81
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: Patent No. US20020177164A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
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: APPLICANT: Napier, Mary A.
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: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
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: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730PIC66
: CURRENT FILING DATE: 2001-11-20
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Query Match 27.2%; Score 28; DB 10; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 5 TGAAGTGAATACAGCATTAAATAGTCTGATATGTGAATTCCTATA 64  
DB 216 TGAAGTGTGTTAAATCTTCAATGCGGATAAATACAGCTGCATCTGATTAATCCACCA 157  
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DB 156 CCGTGTAAAAATAGTA 140

## RESULT 29

;; Sequence 106, Application US/09989735  
;; Publication No. US20020193299A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
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;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kijavini, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC61  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 10; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 5 TGACTGGAATACAGTTTATGACGATTAATAGCTCCGCAATGTGATTCCTATA 64  
DB 216 TGAGTGGTTTAAATCTTTCATGGTGGATAAATACAGTCGATCTATGATATCCACCA 157  
QY 65 CAGTTAAAAAACGTA 81  
DB 156 CCCTGTAAAAATATGTA 140

RESULT 30  
US-09-990-444-106/C  
; Sequence 106, Application US/09990444  
; Publication No. US20020193300A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Matanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C19

;; CURRENT APPLICATION NUMBER: US/09/990,444  
;; CURRENT FILING DATE: 2001-11-14  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/062250  
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;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
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;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 10; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 5 TGACGTGAATACAGCTTAATGACAGCATTAAATGCTCGATATGTAATGCTAATA 64  
Db 216 TGAGTGTGTTAAATCTTCATGCTGGATAAATACAGCTGATATGATATATCCACCA 157  
OY 65 CAGTTAAAAAACGCTA 81  
Db 156 CCCTGTAAAAAATAGTA 140

RESULT 31  
US-09-991-181-106/c  
; Sequence 106, Application US/09991181  
; Publication No. US20020197615A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Bolstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijaviv, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730PIC53  
; CURRENT APPLICATION NUMBER: US/09/991,181  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/049787

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3	PRIOR APPLICATION NUMBER: 60/089512
4	PRIOR FILING DATE: 1998-06-16
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54	PRIOR FILING DATE: 1998-06-25
55	PRIOR APPLICATION NUMBER: 60/090690
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;; PRIOR FILING DATE: 1998-06-26  
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;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 10; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 5 TCACGAGATACAGTTTATGACAGCATTAATAGCTCTGCATATGTAATGCTAATA 64  
DB 216 TTAGGGTTTAATATCTTTCATGTGTGGATTAATACAGCTGCATATGATATATCCACCA 157  
QY 65 CAGTTAAAAAAGCGTA 81  
DB 156 CCGCTGTAATAATACTA 140

RESULT 32  
US-09-989-730-106/c  
;; Sequence 106, Application US/09989730  
;; Publication No. US20020197674A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Guiney, Austin L.  
;; APPLICANT: Kijavlin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
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;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C69  
CURRENT APPLICATION NUMBER: US/09/989,730  
PRIOR FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17

;; PRIOR APPLICATION NUMBER: 60/065186  
;; PRIOR FILING DATE: 1997-11-12  
;; PRIOR APPLICATION NUMBER: 60/065311  
;; PRIOR FILING DATE: 1997-11-13  
;; PRIOR APPLICATION NUMBER: 60/066770  
;; PRIOR FILING DATE: 1997-11-24  
;; PRIOR APPLICATION NUMBER: 60/075945  
;; PRIOR FILING DATE: 1998-02-25  
;; PRIOR APPLICATION NUMBER: 60/078910  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/083322  
;; PRIOR FILING DATE: 1998-04-28  
;; PRIOR APPLICATION NUMBER: 60/084600  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/087106  
;; PRIOR FILING DATE: 1998-05-28  
;; PRIOR APPLICATION NUMBER: 60/087607  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/087609  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/087759  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/087827  
;; PRIOR FILING DATE: 1998-06-03  
;; PRIOR APPLICATION NUMBER: 60/088021  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088025  
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;; PRIOR APPLICATION NUMBER: 60/088026  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088028  
;; PRIOR FILING DATE: 1998-06-04  
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;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088033  
;; PRIOR FILING DATE: 1998-06-04  
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;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088167  
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;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088212  
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;; PRIOR APPLICATION NUMBER: 60/088217  
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;; PRIOR APPLICATION NUMBER: 60/088734  
;; PRIOR FILING DATE: 1998-06-10  
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;; PRIOR APPLICATION NUMBER: 60/088826  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088858  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/088861  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/088876  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/089105  
;; PRIOR FILING DATE: 1998-06-12  
;; PRIOR APPLICATION NUMBER: 60/089440  
;; PRIOR FILING DATE: 1998-06-16  
;; PRIOR APPLICATION NUMBER: 60/089512

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1      PRIOR APPLICATION NUMBER: 60/091360
2      PRIOR FILING DATE: 1998-07-01
3      PRIOR APPLICATION NUMBER: 60/091478
4      PRIOR FILING DATE: 1998-07-02
5      PRIOR APPLICATION NUMBER: 60/091544
6      PRIOR FILING DATE: 1998-07-01
7      PRIOR APPLICATION NUMBER: 60/091519
8      PRIOR FILING DATE: 1998-07-02
9      PRIOR APPLICATION NUMBER: 60/091626
10     PRIOR FILING DATE: 1998-07-02
11     PRIOR APPLICATION NUMBER: 60/091633
12     PRIOR FILING DATE: 1998-07-02
13     PRIOR APPLICATION NUMBER: 60/091978
14     PRIOR FILING DATE: 1998-07-07
15     PRIOR APPLICATION NUMBER: 60/091982
16     PRIOR FILING DATE: 1998-07-07
17     PRIOR APPLICATION NUMBER: 60/092182
18     PRIOR FILING DATE: 1998-07-09
19
20 Query Match      27.2%  Score 28;  DB 10;  Length 466;
21 Best Local Similarity      59.7%  Pred. No. 53;
22 Matches      46;  Conservative      0;  Mismatches      31;  Indels      0;  Gaps      0
23
24 QY      5      TGACTGGAATAACAGTTTAATGACACGCAATTAATACCTCTCGATATGCAATTCGTAATA 64
25      111 111 11 1111111 1111111 1111111 111111 111111 111111 111111
26 Db      216      TGAGCGGTTTAAATCTTTCATGCTGGATTAATAATACAGCTCATCTATGATATATCCACCA 157
27
28 QY      65      CAGTTAAAAAAGCGTA 81
29      1 1111111 111
30 Db      156      CCTGTAAAAAATAGTA 140
31
32 RESULT 33
33 US-09-990-436-106/c
34 Sequence 106, Application US/09990436
35 Publication No. US20020198148a1
36
37 GENERAL INFORMATION:
38
39 APPLICANT: Ashkenazi, Avi J.
40 APPLICANT: Baker, Kevin P.
41 APPLICANT: Botstein, David
42 APPLICANT: Desnoyers, Luc
43 APPLICANT: Eaton, Dan L.
44 APPLICANT: Ferrara, Napoleone
45 APPLICANT: Fong, Sherman
46 APPLICANT: Gerber, Hanspeter
47 APPLICANT: Gerritsen, Mary E.
48 APPLICANT: Goddard, Audrey
49 APPLICANT: Godowski, Paul J.
50 APPLICANT: Grimaldi, J. Christopher
51 APPLICANT: Gurney, Austin L.
52 APPLICANT: Kljavin, Ivar J.
53 APPLICANT: Napier, Mary A.
54 APPLICANT: Pan, James
55 APPLICANT: Paoni, Nicholas F.
56 APPLICANT: Roy, Margaret Ann
57 APPLICANT: Stewart, Timothy A.
58 APPLICANT: Tumas, Daniel
59 APPLICANT: Watanabe, Colin K.
60 APPLICANT: Williams, P. Mickey
61 APPLICANT: Wood, William I.
62 APPLICANT: Zhang, Zhenli
63
64 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
65 FILE REFERENCE: P2730PIC14
66 CURRENT APPLICATION NUMBER: US/09/990,436
67 PRIOR FILING DATE: 2001-11-14
68 PRIOR APPLICATION NUMBER: 60/049787
69 PRIOR FILING DATE: 1997-06-16
70 PRIOR APPLICATION NUMBER: 60/062250
71 PRIOR FILING DATE: 1997-10-17
72 PRIOR APPLICATION NUMBER: 60/065186
73 PRIOR FILING DATE: 1997-11-12
74 PRIOR APPLICATION NUMBER: 60/065311

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[illegible]



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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      27.2%; Score 28; DB 10; Length 466;
Best Local Similarity 59.7%; Pred. No. 53;
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY      5 TCACGTGCAATACAGTTTATGACACGATTAATGCTCCGATATGTCATTGCTTATA 64
         ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      216 TGAGTGGTTTAAATCTTTCATGCTGGATTAATACAGCTCATCTATGTAATCCACCA 157
         ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      65 CAGTTAAAAAACGTA 81
         | | ||| ||| ||| |||
Db      156 CCCTGTAATAAATAGTA 140
         ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 34
US-09-993-687-106/c
; Sequence 106, Application US/09993687
; Publication No. US20020198149A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C11
; CURRENT APPLICATION NUMBER: US/09/993,687
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
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; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
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; PRIOR APPLICATION NUMBER: 60/088212
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; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
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; PRIOR APPLICATION NUMBER: 60/088742
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; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
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; PRIOR APPLICATION NUMBER: 60/088826
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; PRIOR APPLICATION NUMBER: 60/088858
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; PRIOR APPLICATION NUMBER: 60/088876
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; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
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; PRIOR APPLICATION NUMBER: 60/089512
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; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
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;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089598  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089599  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089600  
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;; PRIOR FILING DATE: 1998-06-23  
;; PRIOR APPLICATION NUMBER: 60/090429  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090431  
;; PRIOR FILING DATE: 1998-06-24  
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;; PRIOR APPLICATION NUMBER: 60/090444  
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;; PRIOR APPLICATION NUMBER: 60/090445  
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;; PRIOR APPLICATION NUMBER: 60/090694  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090695  
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;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01

;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 10; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 5 TGACGTGATTAACAGTTTAAATGACAGCATTAATAGCTCCTGCATATGTAATTGCTAATA 64  
DB 216 TGAGTGGTTTAAATCTTTCATGTGGATTAATACAGCTGCATATGATATCCACCA 157  
QY 65 CAGTTAAAAAACGGTA 81  
DB 156 CCCTGTAATAATAGTA 140

RESULT 35  
US-09-989-734-106/c  
; Sequence 106, Application US/09989734  
; Publication No. US20030003531A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C64  
; CURRENT APPLICATION NUMBER: US/09/989,734  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28	PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28	PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02	PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02	PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02	PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03	PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088032
PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05	PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05	PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05	PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05	PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09	PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10	PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10	PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10	PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10	PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11	PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11	PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11	PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12	PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16	PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16	PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16	PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17	PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17	PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17	PRIOR APPLICATION NUMBER: 60/089598

[illegible]

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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      27.2%; Score 28; DB 11; Length 466;
Best Local Similarity 59.7%; Pred. No. 53;
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY      5 TCACGCGATACAGCTTATGACGACATTAATAGCTCCTGCATATGTAATGCTAATA 64
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      216 TGAGGGTTAATCATCTTCATGTGGATTAATACAGCTGCATCATATATACACCA 157
        | | ||| ||| |||

QY      65 CAGTTAAAAACGGTA 81
        | | ||| ||| |||
Db      156 CCCGTGTAATAATAGTA 140

RESULT 36
US-09-997-653-106/c
; Sequence 106, Application US/09997653
; Publication No. US20030008297A1
GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Getzler, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C38
CURRENT APPLICATION NUMBER: US/09/997,653
PRIOR APPLICATION NUMBER: 2001-11-15
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28

; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
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; PRIOR APPLICATION NUMBER: 60/089105
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; PRIOR APPLICATION NUMBER: 60/089440
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; PRIOR APPLICATION NUMBER: 60/089512
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; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
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;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089653  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089801  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/089907  
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;; PRIOR FILING DATE: 1998-06-18  
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;; PRIOR FILING DATE: 1998-06-19  
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;; PRIOR APPLICATION NUMBER: 60/090254  
;; PRIOR FILING DATE: 1998-06-22  
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;; PRIOR FILING DATE: 1998-06-23  
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;; PRIOR FILING DATE: 1998-06-24  
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;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090444  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090445  
;; PRIOR FILING DATE: 1998-06-24  
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;; PRIOR FILING DATE: 1998-06-24  
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;; PRIOR FILING DATE: 1998-06-24  
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;; PRIOR FILING DATE: 1998-06-25  
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;; PRIOR FILING DATE: 1998-07-01  
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;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02

;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09  
Query Match 27.2% Score 28; DB 11; Length 466;  
Best Local Similarity 59.7% Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
OY 5 TGAAGTGAATACAGCTTAATGACGATTAATGCTCCGATATGGAATGCTATA 64  
DB 216 TGAAGTGTAAATCTTCATGTTGGATTAATACAGCTGCTATGATATCCACCA 157  
OY 65 CAGTTAAAAAACGGTA 81  
DB 156 CCCTGTAAAAAATAGTA 140  
RESULT 37  
US-09-993-667-106/c  
; Sequence 106, Application US/09993667  
; Publication No. US20030022187A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C4  
; CURRENT APPLICATION NUMBER: US/09/993,667  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/087106

[illegible]

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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      27.2%; Score 28; DB 11; Length 466;
Best Local Similarity 59.7%; Pred. No. 53;
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY      5  TGACGTGGAATACAGCTTTATGACAGCATTAATAGCTCCTGCATGATGCAATTCGTAATA 64
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      216 TGAGTGGTTNAATCTTTCATGCGATGAATAACAGCTGCATCTATGTAATCCACCA 157
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      65  CAGTTAAAAACGGTA 81
        | | ||||| |||
DB      156 CCCTGTAAAAAATAGTA 140
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 38
US-09-997-428-106/c
; Sequence 106, Application US/09997428
; Publication No. US20030027162A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guirney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C44
; CURRENT APPLICATION NUMBER: US/09/997,428
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
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; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
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; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
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; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
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; PRIOR FILING DATE: 1998-06-17
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
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Query Match          27.2%;   Score 28;   DB 11;   Length 466;
Best Local Similarity 59.7%;   Pred.No. 53;
Matches 46;   Conservative 0;   Mismatches 31;   Indels 0;   Gaps 0

QY      5 TGACGGAATTAACAGCTTTAATGACAGCATTATAGCTCCTGCATATGGAATTGCTAATA 64
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db      216 TGAGTGAGTAAATACCTTATGATGAGGATTAATAACAGCTGATCTATGATTAATCCACCA 157
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111

QY      65 CAGTTAAAAAACGCTA 81
      1 111111 111
Db      156 CCTGTAAAAAATACTA 140
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111

RESULT 39
US-09-997-666-106/C
; Sequence 106, Application US/09997666
; Publication No. US20030027163A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrata, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301PC42
; CURRENT APPLICATION NUMBER: US/09/997,666
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759

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Query Match	27.28;	Score 28;	DB 11;	Length 466;
Best Local Similarity	59.78;	Pred. No. 53;		

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Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
OY 5 TGACGTGAATACACGTTTATGACACCATTAATAGCTCCGATGATGATGCTAATA 64
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Db 216 TGAGTGGTTTAAATCTTCATGCTGGATTAATAACAGCGCATCATGATATCCACCA 157
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 65 CAGTTAAAAAACGGTA 81
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 156 CCCTGTAAAAAATAGTA 140
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 40
US-09-990-438-106/C
; Sequence 106, Application US/09990438
; Publication No. US2003002754A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC3
; CURRENT APPLICATION NUMBER: US/09/990,438
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
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; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
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; PRIOR APPLICATION NUMBER: 60/087609
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; PRIOR FILING DATE: 1998-06-02
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; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
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; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
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; PRIOR APPLICATION NUMBER: 60/088212
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; PRIOR FILING DATE: 1998-06-10
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;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 11; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
QY 5 TGACGTGAATACAGTTTAATGACAGCATTAATAGCTCCGTCATATGTAATGCTATATA 64

Db 216 TGAGTGGTTAAATCTTCAATGCGGATTAATAACAGCTGCACTATGATATCCACCA 157  
QY 65 CAGTTAAAAAACGGTA 81  
Db 156 CCCTGTAAAAAATAGTA 140

RESULT 41  
US-09-990-562-106/c  
; Sequence 106, Application US/09990562  
; Publication No. US20030027985A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Bolstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavyn, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watnabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C18  
; CURRENT APPLICATION NUMBER: US/09/990,562  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
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Query Match 27.2%; Score 28; DB 11; Length 466;  
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Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 5 TGACGTGAGATTAACGATTATATGACGATTAATGCTCTGCAATATGATTCGTATA 64  
DB 216 TGACGTGATTAAATCTTTCATGCTGCGATTAATACAGCTGCACTCATGTATGATTAATCCACCA 157

OY 65 CAGTAAAAAACGTA 81  
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Db 156 CCCTGTAATAATAGTA 140

RESULT 42  
US-09-990-711-106/c  
; Sequence 106, Application US/09990711  
; Publication No. US2003003202A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan L.  
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; APPLICANT: Goddard, Audrey  
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; APPLICANT: Napier, Mary A.  
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; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
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; APPLICANT: Tumas, Daniel  
; APPLICANT: Matanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC2  
; CURRENT APPLICATION NUMBER: US/09/990,711  
; PRIOR APPLICATION NUMBER: 2001-11-14  
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PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 11; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 5 TGACGAGATACAGTAAATGACAGCATTAATAGCTCTCGATGTGGAATGCTAATA 64  
DB 216 TGAGGAGTTNAATTTTTCATGGTGAGTAATAACAGCTGCATGTATGATATCCACCA 157  
OY 65 CAGTTAAAAAAGCGTA 81  
DB 156 CCGTGTAAAAAATAGTA 140

RESULT 43  
US-09-989-726-106/c  
; Sequence 106, Application US/09989726  
; Publication No. US20030040473A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerltsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Guirney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC60  
; CURRENT APPLICATION NUMBER: US/09/989,726  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
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53	PRIOR FILING DATE: 1998-07-01
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55	PRIOR FILING DATE: 1998-07-02
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57	PRIOR FILING DATE: 1998-07-02
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59	PRIOR FILING DATE: 1998-07-02
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62	PRIOR APPLICATION NUMBER: 60/09198282
63	PRIOR FILING DATE: 1998-07-07
64	PRIOR APPLICATION NUMBER: 60/09218222
65	PRIOR FILING DATE: 1998-07-09

Query Match	27.2%	Score 28;	DB 11;	Length 466;
Best Local Similarity	59.7%	Pred. No. 53;		
Matches 46; Conservative	0;	Mismatches 31;	Indels	

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          | | | | | | | | | | | | | | |  
Db     216 TGAAGTGTTNNAATCTTTCATGCGTGGCATTAATACGAGCTGCATCTATGCATTAATCCACA 15

Qy 65 CAGTTAAAAAACGGTA 81  
| | | | | | | |  
Db 156 CCCTGTAAAAAATAGTA 140

## RESULT 44

US-09-998-156-106/C  
Sequence 106, Application US/09998156  
Publication No. US20030044806A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC28  
CURRENT APPLICATION NUMBER: US/09/998,156  
CURRENT FILING DATE: 2001-11-15  
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PRIOR APPLICATION NUMBER: 60/090254  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090349  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090355







GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2003, 06:50:58 ; Search time 1644 Seconds

(without alignments)  
1522.726 Million cell updates/sec

Title: US-09-693-205A-7\_COPY\_6543\_6645

Perfect score: 103  
Sequence: 1 gaagtagcagcgaataacagf.....tccctgtctgtatccaaca 103

Scoring table: IDENTITY\_NUC

Gapop 60.0 ; Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
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3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
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24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
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27: em\_gss\_vtl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	55.2	53.6	758	12	AL710553 DKFZp686L
4	55.2	53.6	1010	12	BM989861 UI-H-D10-BM472954
					BM472954 AGENCOURT

5	55.2	53.6	1083	12	BM476887	BM476887 AGENCOURT
6	46.2	44.9	1123	13	B0517082	B0517082 AGENCOURT
7	37.6	36.5	491	13	B0955705	B0955705 AGENCOURT
8	37.6	36.5	518	9	A1445627	A1445627 tJ08c05.x
9	36.2	35.1	256	12	BG898417	BG898417 HOA8-1-G1
10	36.2	35.1	507	9	A1652546	A1652546 wb61e01.x
11	36.2	35.1	534	9	A1742206	A1742206 wg39b09.x
12	36.2	35.1	607	14	CA437823	CA437823 UI-H-DHO-
13	36.2	35.1	632	13	B0772275	B0772275 UI-H-E21-
14	34.8	33.8	807	29	CNS023X0	AL180045 Telradcon
15	34	33.0	610	9	AV404852	AV404852 AV404852
16	33.8	32.8	464	14	N34305	N34305 Y51h10.s1
17	32.2	31.3	775	9	AU003905	AU003905 AU003905
18	31.8	30.9	689	29	BX242269	BX242269 Danilo rer
19	31.8	30.9	760	28	BH979420	BH979420 cdf92a01.
20	31.6	30.7	858	28	B2978614	B2978614 PUG1887D
21	31.6	30.7	1088	29	B264543	B264543 CH230-458
22	31.4	30.5	802	10	BG187125	BG187125 R576108 A
23	31	30.1	406	12	B1475987	B1475987 fp51a12.x
24	31	30.1	520	12	B1673496	B1673496 f43905.x
25	31	30.1	570	12	BM082805	BM082805 fu26910.x
26	31	30.1	576	29	BX192053	BX192053 Danilo rer
27	30.8	29.9	175	28	AZ060239	AZ060239 RPCI-23-4
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32	30.6	29.7	509	28	AQ242919	AQ242919 HS_2061_A
33	30.6	29.7	525	28	AQ390562	AQ390562 CTRBI-E1-
34	30.6	29.7	704	29	B2220889	B2220889 CH230-271
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42	30	29.1	382	28	BH002214	BH002214 BMAC02E1
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## ALIGNMENTS

RESULT 1  
AA897178/c 238 bp mRNA linear EST 04-JAN-1999  
LOCUS am09e08.s1 Soares\_NFL\_T-GBC\_S1 Homo sapiens cDNA clone  
IMAGE:1466342 3', mRNA sequence.  
ACCESSION AA897178  
VERSION AA897178.1 GI:3033798  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 238)  
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 847 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 132.  
location/Qualifiers  
1..238  
/organism="Homo sapiens"

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/clone="IMAGE:1466342"
/lab_host="DH10B"
/clone_lib="Soares.NFL.T.GBC.S1"
/notes="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19, testis NT, and B-cell
NCI.CGAP.GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT      71 a      53 c      45 g      69 t
ORIGIN
Query Match      53.6%; Score 55.2; DB 9; Length 238;
Best Local Similarity 75.0%; Pred. No. 3.6e-05;
Matches 69; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY      1 GAAGTACTGGAATACAGTTTAATGACAGCATTAATAGCTCGATATGCAATTGCT 60
        |||||||
DB      150 GAAGTACACGAGTAATACAGTTTAATGACAGCATTAATAGCTCGATATGCAATTGCT 91
QY      61 AATACAGTTAAAAAAGCGTATTTCCCTGCTT 92
        | | | | | | | | | | | | | | | | | |
DB      90 TAATACAGTTAAAAAAGCGTATTTCCCTGCT 59

RESULT 2
AL710553      713 bp      mRNA      linear      EST 22-MAR-2002
LOCUS      DKFZP666L236_R1 686 (synonym: h1cc3) Homo sapiens cDNA clone
DEFINITION      DKFZP666L236 5', mRNA sequence.
ACCESSION      AL710553
VERSION      AL710553.1 GI:19693908
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 713)
AUTHORS      Ansorge,W., Winkner,U., Mewes,W., Well,B. and Wiemann,S.
TITLE      EST (Ansorge,W., Winkner,U., Mewes,H.W., Well,B. and Wiemann,S.)
JOURNAL      Unpublished
COMMENT      Contact: Ansorge W
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No s1 sequence available.
This clone (DKFZP666L236) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source
1..713
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="DKFZP666L236"
/issue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: h1cc3)"
/notes="Vector: pT73D-Pac, Site_1: SfiI, Site_2: SfiIb;
location/Qualifiers

```

```

BASE COUNT      211 a      140 c      129 g      233 t
ORIGIN
Query Match      53.6%; Score 55.2; DB 9; Length 713;
Best Local Similarity 75.0%; Pred. No. 4.3e-05;
Matches 69; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY      1 GAAGTACTGGAATACAGTTTAATGACAGCATTAATAGCTCGATATGCAATTGCT 60
        |||||||
DB      159 GAAGTACACGAGTAATACAGTTTAATGACAGCATTAATAGCTCGATATGCAATTGCT 218
QY      61 AATACAGTTAAAAAAGCGTATTTCCCTGCTT 92
        | | | | | | | | | | | | | | | | | |
DB      219 TAATACAGTTAAAAAAGCGTATTTCCCTGCT 250

RESULT 3
BM989861      758 bp      mRNA      linear      EST 17-JUN-2002
LOCUS      UI-H-DIO-ato-m-19-0-UI.s1 NCI.CGAP_DIO Homo sapiens cDNA clone
DEFINITION      IMAGE:5862330 3', mRNA sequence.
ACCESSION      BM989861
VERSION      BM989861.1 GI:19709250
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 758)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL      Tumor Gene Index
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
Seq primer: M13 FORWARD
POLY-A=yes.
FEATURES
source
1..758
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:5862330"
/issue_type="Lung Focal Fibrosis"
/dev_stage="Adult"
/clone_lib="NCI.CGAP.DIO"
/notes="Organ: lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI.CGAP.DIO is a cDNA library containing the following
tissue(s): A pool of lung Focal Fibrosis. The library was
constructed according to Bonaldi, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
ATACCGGCTC.
TAG_LIB=UI-H-DIO
TAG_TISSUE=Lung with fibrosis
TAG_SEQ=ATACCGGCTC"
BASE COUNT      215 a      144 c      136 g      263 t
ORIGIN

```



CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM14090 row: d column: 14  
High quality sequence start: 49  
High quality sequence stop: 267.  
Location/Qualifiers

## FEATURES

source

1. 1123  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6514621"  
/tissue\_type="leiomyosarcoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_71"  
/note="Organ: uterus; Vector: pCMV-Sport6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 2.1 kb."  
BASE COUNT 283 a 336 c 194 g 310 t  
ORIGIN

Query Match 44.9%; Score 46.2; DB 13; Length 1123;  
Best Local Similarity 94.1%; Pred. No. 0.015;  
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GAAGTACTGATTAACAGTTTAATGACAGCATTAATAGCTCCTGCATATG 51  
|||||  
Db 313 GAAGTACTGATTAACAGTTTAATGACAGCATTAATAGCTCCTGCATATG 363

RESULT 7  
BU955705/c 491 bp mRNA linear EST 21-OCT-2002  
LOCUS AGENCOURT.10612800 NIH\_MGC\_126 Homo sapiens CDNA clone  
DEFINITION IMAGE:6727961 5', mRNA sequence.  
ACCESSION BU955705  
VERSION BU955705.1 GI:24185277  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
REFERENCE NIH-MGC <http://mhc.nci.nih.gov/>.  
1 (bases 1 to 491)  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: NCI  
CDNA Library Preparation: Michael Brownstein Laboratory  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LDCM3048 row: m column: 16  
High quality sequence stop: 464.  
Location/Qualifiers

## FEATURES

source

1. 491  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6727961"  
/tissue\_type="mixed (pool of 40 RNAs)"  
/lab\_host="DH10B (T1-phage-resistant)"  
/clone\_lib="NIH\_MGC\_126"  
/note="Vector: pDNR-LIB; Site\_1: SfiI (ggccattatggcc);  
Site\_2: SfiI (ggccgctcggcc); Double-stranded cDNA was  
prepared from a pool of 40 cell line polyA+ RNAs (bladder  
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -  
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,

kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,  
ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary  
gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were  
used in cloning as follows:  
5'-AAGCAGCGTATCAAGCCAGACAGCGCCATAGCGCCGGC-3' and  
5'-ATTCGTAGAGCGCGAGCGCGCCGACATG-dT(30)NN-3'. Full-length  
created library was constructed using the Clontech  
Creator SMART kit and size-selected to contain the 0.5-1  
kb size fraction (other fractions present in NIH\_MGC\_127  
and NIH\_MGC\_128). Library created in the laboratory of T.  
Udgin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH\_MGC  
Library."

BASE COUNT 161 a 75 c 81 g 159 t 15 others  
ORIGIN

Query Match 36.5%; Score 37.6; DB 13; Length 491;  
Best Local Similarity 61.0%; Pred. No. 3.1;  
Matches 61; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

OY 1 GAAGTACTGATTAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTAATGCT 60  
|||||  
Db 129 GGAAGACACAAAAAATAATTCAGCATTAAGACCCCTAGAGACTTACTTTCT 70  
OY 61 AATACGTTAAAAACGATTTCCCTGCTGTGATCCA 100  
|||||  
Db 69 AATCAATTAATAAAAAAGGCTTTCAGTACTTCTCATCTA 30

RESULT 8  
A1445627 518 bp mRNA linear EST 13-APR-1999  
LOCUS t308c05.x1 NCI-CGAP\_Gas4 Homo sapiens CDNA clone IMAGE:2140904 3',  
DEFINITION mRNA sequence.  
ACCESSION A1445627  
VERSION A1445627.1 GI:4289534  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
1 (bases 1 to 518)  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
JOURNAL Tumor Gene Index  
COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov/btbp/image/image.html>  
Insert Length: 227 Std Error: 0.00  
Seq primer: -40up from Gibco  
High quality sequence stop: 424.  
Location/Qualifiers

## FEATURES

source

1. 518  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2140904"  
/tissue\_type="poorly differentiated adenocarcinoma with  
signed ring cell features"  
/lab\_host="DH10B"  
/clone\_lib="NCI-CGAP\_Gas4"  
/note="Organ: stomach; Vector: pCMV-Sport6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.69 kb. Life Technologies catalog #:  
11549-011"  
BASE COUNT 182 a 89 c 85 g 162 t

ORIGIN

Query Match 36.5% Score 37.6; DB 9; Length 518;  
 Best Local Similarity 61.0%; Pred. No. 3.1;  
 Matches 61; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 GAAGTGCATGATAACAGTTTAATGACAGCATTAAATAGCTCCGATATGTGAATGCT 60  
 373 GGAAGACACAAAAAATAATCCAGCATTCAGAACCCAGAGACTTACTTTCT 432

Db 61 AATACAGTTAAAAAACGCTATTTCCCTGGTTCGATCCA 100  
 433 AATCAATTAAAAAAGGTCTTTCAGTACTTCTCATCTA 472

RESULT 9  
 BG898417/c 256 bp mRNA linear EST 06-NOV-2001  
 LOCUS HOA8-1-G11 HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA,  
 mRNA sequence.  
 ACCESSION BG898417.1 GI:14308666  
 VERSION BG898417.1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
 Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
 Lark,M.W.  
 Identification and initial characterization of 5000 expressed  
 sequenced tags (ESTs) each from adult human normal and  
 osteoarthritic cartilage cDNA libraries  
 Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
 JOURNAL MEDLINE 21482651  
 PUBMED 11597177  
 COMMENT Contact: Sanjay Kumar  
 UW2109  
 GlaxoSmithKline  
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
 Tel: 610-270-7245  
 Fax: 610-270-5598  
 Email: sanjay.kumar-legsk.com  
 Seq primer: T7

FEATURES  
 Location/Qualifiers  
 1..256  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /tissue\_type="cartilage"  
 /lab\_host="E.coli DH10 B"  
 /clone\_lib="HOA (Human Osteoarthritic Cartilage)"  
 /note="Vector: pSPORT I; Site\_1: SalI; Site\_2: NotI;  
 Directional"

BASE COUNT 61 a 56 c 54 g 85 t

ORIGIN

Query Match 35.1% Score 36.2; DB 12; Length 256;  
 Best Local Similarity 62.9%; Pred. No. 6.6;  
 Matches 56; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 12 AATAACAGTTTATGACAGCATTAAATGCTCCGCAATATGCAATTCCTAATACAGTTAA 71  
 234 AAAAAAATAATTAATCCAGCATTCAGAACCCAGAGACTTACTTTCTAATCAATTAA 175

Db 72 AAAAAGGTATTTCCCTGGTTCGATCCA 100  
 174 AAAAAAGTCTTTCAGTACTTCTCATCTA 146

RESULT 10  
 A1652546

LOCUS A1652546 507 bp mRNA linear EST 17-DEC-1999  
 DEFINITION wp1601.x1 NCI-CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2310168 3',  
 mRNA sequence.  
 ACCESSION A1652546  
 VERSION A1652546  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
 Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
 Lark,M.W.  
 Identification and initial characterization of 5000 expressed  
 sequenced tags (ESTs) each from adult human normal and  
 osteoarthritic cartilage cDNA libraries  
 Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
 JOURNAL MEDLINE 21482651  
 PUBMED 11597177  
 COMMENT Contact: Sanjay Kumar  
 UW2109  
 GlaxoSmithKline  
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
 Tel: 610-270-7245  
 Fax: 610-270-5598  
 Email: sanjay.kumar-legsk.com  
 Seq primer: T7

FEATURES  
 Location/Qualifiers  
 1..507  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2310168"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI-CGAP\_GC6"  
 /note="Vector: pT77AD-Pac (Pharmacia) with a modified  
 polylinker. Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA  
 from the normalized library NCI-CGAP\_GC4 was prepared, and  
 ss circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (cloneds  
 1257096-1258631, 1459064-1470983, and 1475592-1476743).  
 Subtraction by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 174 a 88 c 85 g 159 t

ORIGIN

Query Match 35.1% Score 36.2; DB 9; Length 507;  
 Best Local Similarity 62.9%; Pred. No. 7.5;  
 Matches 56; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 12 AATAACAGTTTATGACAGCATTAAATGCTCCGCAATATGCAATTCCTAATACAGTTAA 71  
 381 AAAAAAATAATTAATCCAGCATTCAGAACCCAGAGACTTACTTTCTAATCAATTAA 440

Db 72 AAAAAGGTATTTCCCTGGTTCGATCCA 100  
 441 AAAAAAGTCTTTCAGTACTTCTCATCTA 469

RESULT 11  
 A1742206 534 bp mRNA linear EST 19-DEC-1999  
 LOCUS wq39b09.x1 Soares NSF\_F8\_9W\_OT\_PA\_S1 Homo sapiens cDNA clone  
 IMAGE:2367449 3', mRNA sequence.  
 ACCESSION A1742206  
 VERSION A1742206.1 GI:5110494  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 534)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
This clone is available royalty-free through LNLN; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Insert Length: 789 Std Error: 0.00  
Seq primer: -40UP from Glibco  
High quality sequence stop: 452.

FEATURES  
source  
1. 534  
Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2367449"  
/lab\_host="PH10B"  
/clone\_lib="Soares-NSF-F8-9W-OT\_PA\_P-S1"  
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and clones: Soares NbHSF pool 1: 309384-310919, 323208-325895 Soares NbZHP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares NbZHF-9W pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 304776-306311, 320136-322823, 326280-326653 Soares NbHOR pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Ronaldo."

BASE COUNT 185 a 89 c 86 g 174 t  
ORIGIN

Query Match 35.1%; Score 36.2; DB 9; Length 534;  
Best Local Similarity 62.9%; Pred. No. 7.6;  
Matches 56; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 12 AATAACAGTTAATGACAGCATTAAATAGCTCGATATGTAATGTAATACAGTTAA 71  
DB 397 AAAAAAAAAAATTCACAGCATTCAAGACCTAGAGACTTCTTCAATCAATTAA 456  
QY 72 AAAAAAGTATTTCCCTGGTCTGATCCA 100  
DB 457 AAAAAAGTCTTCACTACTCTCATCTA 485

RESULT 12  
CA437823 607 bp mRNA linear EST 08-NOV-2002  
LOCUS  
DEFINITION UI-H-DHO-aur-o-23-0-UI.s1 NCI-CGAP\_DHO Homo sapiens cDNA clone  
ACCESSION CA437823  
VERSION  
KEYWORDS  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 607)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. Jose Mercuende  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
DNA Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
The following repetitive elements were found in this cDNA sequence: 1-36, >AT\_richlow\_complexity (matched complement)  
Seq primer: M13 FORWARD  
POLYA-yes.

FEATURES  
source  
1. 607  
Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-DHO-aur-o-23-0-UI"  
/tissue\_type="Metastatic Chondrosarcoma"  
/dev\_stage="Adult"  
/lab\_host="NCI-CGAP-DHO"  
/clone\_lib="NCI-CGAP-DHO"  
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; NCI-CGAP-DHO is a cDNA library containing the following tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGATCATTTGC.  
TAG LIB=UI-H-DHO  
TAG-TRISSE=Lung  
TAG-SEQ=AGATCATTTGC"

BASE COUNT 210 a 94 c 99 g 204 t  
ORIGIN

Query Match 35.1%; Score 36.2; DB 14; Length 607;  
Best Local Similarity 62.9%; Pred. No. 7.8;  
Matches 56; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 12 AATAACAGTTAATGACAGCATTAAATAGCTCGATATGTAATGTAATACAGTTAA 71  
DB 357 AAAAAAAAAAATTCACAGCATTCAAGACCTAGAGACTTCTTCAATCAATTAA 416  
QY 72 AAAAAAGTATTTCCCTGGTCTGATCCA 100  
DB 417 AAAAAAGTCTTCACTACTCTCATCTA 445

RESULT 13  
B0772275 632 bp mRNA linear EST 26-JUL-2002  
LOCUS  
DEFINITION UI-H-E21-bd1-k-24-0-UI.s1 NCI-CGAP-Ch2 Homo sapiens cDNA clone  
ACCESSION B0772275  
VERSION  
KEYWORDS  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 632)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Steven Gitellis/ Rush Presbyterian, Dept. of



FEATURES	Location/Qualifiers
source	1. .632

BASE COUNT	ORIGIN
217	a TAG_L1B=01-H-EZ1 TAG_TISSUE=grade-2-Chondrosarcoma TAG_SEQ=ATCTAATAG"
104	c
105	g
205	t
1	others

QY	Db	QY	Db
12	400	72	460
AAATACGTTTAAATGACAGCATTAATAGCTCTCATATGGAAATGGTATACGTAA	AAAAAANAATCCAGCATTCAAAGACCTTAGAGACTTACTTTTATCAATTAA	AAAAACGGTATTCCTCGTTCATCA	AAAAACGGTCTTCAGTACTTCATCA
71	459	100	488

RESULT 14	CNS023X0/c	LOCUS	DEFINITION
	CNS023X0	807 bp	DNA
			linear
			GSS 01-SEP-2000
			Tetradon nigroviridis genome survey sequence T7 end of clone
			233B02 of library G from Tetradon nigroviridis, genomic survey
			sequence.

ACCESSION	AL180045
VERSION	AL180045.1
KEYWORDS	GSS: genome survey sequence
SOURCE	Tetradodon nigroviridis
ORGANISM	Tetradodon nigroviridis

## REFERENCE AUTHORS

TITLE	Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL	Nat. Genet. 25 (2), 235-238 (2000)

**TITLE** Characterization and repeat analysis of the compact genome of the freshwater pufferfish *Tetraodon nigroviridis*  
**JOURNAL** Genome Res. 10 (7), 939-949 (2000)

MEDLINE	20359837
PUBMED	10899143
REFERENCE	3 (bases 1 to 807)

Genoscope - Centre National de Séquençage :  
Submitted (12-APR-2000)  
Direct Submission  
Genoscope.  
AUTHORS  
JOURNAL

**COMMENT**

scale clone-end sequencing project of the tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES	Location/Qualifiers
source	1. .807

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/organism="Tetrahodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="233B02"
/clone_1b="G"
/note="Genoscope sequence ID : C0AG233D01Pl-end : T7"
BASE COUNT      167 a      167 g      238 t      32 others
ORIGIN

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Query Match	33.8%;	Score 34.8;	DB 29;	Length 807;
Best Local Similarity	66.7%;	Pred. No. 20;		
Matches	48;	Conservative	1;	Mismatches 23; Indels 0

Qy 5 TGACGTGGAATTAACAGTTTAATGACACGATTAACTCCTCGATATGTAATGGCTATA 64  
||| : ||| | ||||| ||||| || ||| |||  
Db 221 TGACAGKAAATTAGAGTGTAAATGACACATTAACTAGCCCCCTTAAAGAACAACTGTTAGAA 1622

Qy	65	CAGTTAA	76
		↑	
Db	161	AACCTAA	150

RESULT 15  
AV404852

LOCUS	610 bp	mRNA	Linear
DEFINITION	AV404852	Bombyx mori prothoracic gland p50 5th-Inst	
	AV404852	Bombyx mori CDNA clone prgv0517 T3, mRNA sequence	

ACCESSION	AV404852	GI:6908940
VERSION	AV404852.1	
KEYWORDS	EST.	
SOURCE	Bombix mori	(domestic silkworm)
ORGANISM	Bombix mori	

REFERENCE  
1 (bases 1 to 610)

AUTHORS Mita, K., Moriyomo, M., Shimada, T., Okano, K. and Maeda, S  
 TITLE Bombyx mori cDNA  
 JOURNAL Unpublished  
 COMMENT Contact: Mita K

Genome Research Group  
National Institute of Agrobiological Sciences  
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan  
Email: kmitadinas.affrc.go.jp  
method: uni-directional, sequence direction: sequenced from T3 primer

(5' -> 3')  
Project='Silkwork Genome Program in MAF, and Research for the  
Future Program in JSPS', see 'Silkbase',  
<http://www.ab.a.u.-tokyo.ac.jp/silkbase/>, for whole ESTdb.  
Location/Qualifiers

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/mol\_type="mRNA"  
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/clone="p9y0517"  
/sex="female/male mixed"  
/tissue\_type="prothoracic gland"  
/dev\_stage="5th-instar day-4 larva"  
/clone\_lib="Bombyx mori prothoracic gland p50 5th-instar day-4 larva"  
BASE COUNT 216 a 95 c 106 g 192 t 1 others  
ORIGIN  
Query Match 33.0%; Score 34; DB 9; Length 610;  
Best Local Similarity 63.4%; Pred. No. 32;  
Matches 52; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
QY 14 TAACAGTTAATGACGATTAATAGCTCCTCATATGCAATGCTAATGAGTTAAAA 73  
1 TAGCTAATTAATGTAAGCAATATATGTCATATGAAAGTCCCTATCCGTCAG 60  
Db 74 AAGCGTATTTCCCTGGTCTG 95  
61 GGACGTTTGTCTGTGTTTG 82  
RESULT 16 464 bp mRNA linear EST 16-JAN-1996  
N34305  
LOCUS y51h10.s1 Soares multiple sclerosis 2NBHMSF Homo sapiens cDNA  
DEFINITION clone IMAGE:277123 3', mRNA sequence.  
ACCESSION N34305  
VERSION N34305.1 GI:1155447  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 464)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.  
The WashU-Merck EST Project.  
Unpublished  
JOURNAL  
COMMENT  
TITLE  
JOURNAL  
COMMENT  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 402  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: ml3 -40 forward  
High quality sequence stop: 402.  
Location/Qualifiers  
1..464  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:3895499"  
/db\_xref="taxon:9606"  
/clone="IMAGE:277123"  
/sex="male"  
/tissue\_type="multiple sclerosis lesions"  
/dev\_stage="Age 46"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares multiple sclerosis 2NBHMSF"  
/note="Vector: pT73D (Pharmacia) with a modified  
polylinker V type; phagemid; Site\_1: Not I; Site\_2: Eco RI  
; 1st strand cDNA was primed with a Not I - Oligo(dT)"

primer [5'  
TGTTACCAATCTGAAGTGGAGGAGCGCCGATTTTTTTTTTTTTTTT 3']  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT73 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M. Fatima Bonaldi. RNA from 4 multiple sclerosis  
lesions from one patient was kindly provided by Dr. Kevin  
G. Becker (NINDS/NIH)."  
BASE COUNT 164 a 79 c 77 g 144 t  
ORIGIN  
Query Match 32.8%; Score 33.8; DB 14; Length 464;  
Best Local Similarity 60.2%; Pred. No. 34;  
Matches 56; Conservative 0; Mismatches 37; Indels 0; Gaps 0;  
QY 1 GAAGTACTGGAATTAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGCAATGCT 60  
372 GGAAAGACAAAAAATAAATAAATTCAGCATTCAGAACAGCCATGAGACTTACTTCT 431  
Db 61 AATACAGTTAAAAAAGCGTATTTCCCTGGTTC 93  
432 AATCAATTAAAAAAGAGCTTTTCAGTACTTC 464  
RESULT 17 775 bp mRNA linear EST 19-JAN-1999  
AU003905/c  
LOCUS AU003905 Bombyx mori p50(Dalzo) Bombyx mori cDNA clone w800724,  
DEFINITION mRNA sequence.  
ACCESSION AU003905  
VERSION AU003905.1 GI:4161276  
KEYWORDS EST.  
SOURCE Bombyx mori (domestic silkworm)  
ORGANISM Bombyx mori  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
Bombycoidea; Bombycidae; Bombyx.  
REFERENCE 1 (bases 1 to 775)  
Mita, K., Moriyama, M., Shimada, T., Okano, K. and Maeda, S.  
Establishment of cDNA database of Bombyx mori  
Unpublished  
JOURNAL  
COMMENT  
TITLE  
JOURNAL  
COMMENT  
Unpublished  
Contact: Mita K  
Genome Research Group  
National Institute of Agrobiological Sciences  
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan  
Email: kmita@nias.affrc.go.jp  
PROJECT = 'CREST project by JST'.  
Location/Qualifiers  
1..775  
/organism="Bombyx mori"  
/mol\_type="mRNA"  
/strain="p50(Dalzo)"  
/db\_xref="taxon:7091"  
/clone="w800724"  
/clone\_lib="Bombyx mori p50(Dalzo)"  
BASE COUNT 247 a 139 c 151 g 228 t  
ORIGIN  
Query Match 31.3%; Score 32.2; DB 9; Length 775;  
Best Local Similarity 59.1%; Pred. No. 1e+02;  
Matches 55; Conservative 0; Mismatches 38; Indels 0; Gaps 0;  
QY 2 AAGTACGTGGAATTAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGCAATGCTA 61  
94 AAGTAAAAATATATACGCTTACGAAAGTTTAAAAAAGAACATGTAATGTAAT 35  
Db 62 ATACAGTTAAAAAAGCGTATTTCCCTGGTTC 94  
34 TTAATTTAACAAAAACATCAATTTATCTAGTTT 2

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FEATURES
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    Location/Qualifiers
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        /mol_type="genomic DNA"
        /db_xref="taxon:3712"
        /clone_lib="B.oleracea002"
        /note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea T01000DH3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
  BASE COUNT
    264 a 171 c 106 g 219 t
  ORIGIN
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    Best Local Similarity 59.3%; Pred. No. 1.3e+02;
    Matches 54; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
  QY
    13 ATACAGCTTTAATGACAGCATTAATATGTCGATATGTGAATTGCTAATACAGTTAAA 72
      |||| | || |||| |||| |||| | | | |||| |||| | || |
  Db
    157 ATAAATCTTGATGATGAATAAATTAAGTTCATTAATAATATTAATATTAATACATATA 216
      |||| | || |||| |||| |||| | | | |||| |||| | || |
  QY
    73 AAAACGATTTTCCCTGGTCTGTGATCCACA 103
      | || | | | | | | | | | | | | | | | |
  Db
    217 ATAACTCCACTTTCGTGATTCCTTTACAAACA 247
      | || | | | | | | | | | | | | | | | |
  RESULT 20
  B2978614/c
  LOCUS
  DEFINITION
    B2978614 858 bp DNA linear GSS 25-MAR-2003
  ACCESSION
    PUGIJB88TD ZM.0.6_1.0_KB zea mays genomic clone ZMWBTA391008,
  VERSION
    B2978614
  KEYWORDS
    B2978614.1 GI:29207563
  SOURCE
    GSS.
  ORGANISM
    zea mays
    zea mays
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
    clade; Panicoidae; Andropogoneae; Zea.
  REFERENCE
    1 (bases 1 to 858)
    Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Resnick
    A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennetzen,J.
    Maize Genomics Consortium
  TITLE
    Unpublished
  JOURNAL
    Other_GSS: PUGIJB88TB
  COMMENT
    Contact: Cathy Whitelaw
    TIR
    9712 Medical Center Drive, Rockville, MD 20850, USA
    Tel: 301-838-5843
    Fax: 301-838-0208
    Email: whitelaw@etlgr.org
    Seq Primer: TF
    Class: sheared ends.
  FEATURES
    source
      Location/Qualifiers
        1..858
          /organism="Zea mays"
          /mol_type="genomic DNA"
          /strain="B73"
          /db_xref="taxon:4577"
          /clone="ZMWBTA391008"
          /clone_lib="ZM.0.6_1.0_KB"
          /note="Vector: pCR4-topo; Site 1: EcoRI; 0.6-1.0 kb high
          Cot selected genomic DNA library"
  BASE COUNT
    266 a 175 c 157 g 260 t
  ORIGIN
    Query Match 30.7%; Score 31.6; DB 29; Length 858;
    Best Local Similarity 60.5%; Pred. No. 1.6e+02;
    Matches 52; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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	Yy	1	GAGGACGTGCATTAACGGTTTAAAGCAGCATTAATAAGCTCCGCATTATGTGAATTCG	60	
	Dd	242	GTACGATTAAAGCCAAACTATTAATGATGATTATGTAACCGCAATGATCATTTCA	183	
	Yy	61	AATACAGTTAAAAAACCAGTATTTCC	86	
	Dd	182	TATACCGTTTGAAAACCATTAATTC	157	
RESULT 21	BZ264543	1088 bp	DNA	linear	GSS 15-Oct-2002
LOCUS	CH230-458D15.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone				
DEFINITION	CH230-458D15, genomic survey sequence.				
ACCESSION	BZ264543				
VERSION	BZ264543.1	GI:23976989			
KEYWORDS	GSS.				
SOURCE	Rattus norvegicus (Norway rat)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
REFERENCE	1 (bases 1 to 1088)				
AUTHORS	Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M.				
JOURNAL	Rat BAC End Sequences from Library CHORI-230 MbOI segment				
COMMENT	Unpublished Other_GSSs: CH230-458D15.TV Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: szhaoc@tigr.org Clones are derived from the rat BAC library CHORI-230 ( <a href="http://www.chori.org/bacpac/rat230.htm">http://www.chori.org/bacpac/rat230.htm</a> ). For BAC library availability, please contact Pieter de Jong ( <a href="mailto:pdejong@email.cho.org">pdejong@email.cho.org</a> ). Clones may be purchased from BACPAC Resources ( <a href="http://www.chori.org/bacpac/orering_information.htm">http://www.chori.org/bacpac/orering_information.htm</a> ). BAC end page: <a href="http://www.tigr.org/tftp/bac_ends/rat/bac_end_intro.html">http://www.tigr.org/tftp/bac_ends/rat/bac_end_intro.html</a> Plate: 458 row: D column: 15 Seq primer: SP6 Class: BAC ends. Location/Qualifiers 1..1088 /organism="Rattus norvegicus" /mol_type="genomic DNA" /strain="BN/SSNHsd/MCW" /db_xref="taxon:10116" /clone="CH230-458D15" /sex="Female" /cell_type="Brain" /clone_lib="CHORI-230 Segment 2" /note="Vector: PTARPA1.3; Site_1: MboI; Site_2: MboI; CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by Pieter de Jong"				
FEATURES	BASE COUNT	343 a	216 c	163 g	366 t
SOURCE	ORIGIN				
	Query Match	30.7%	Score 31.6;	DB 29;	Length 1088;
	Best Local Similarity	74.1%;	Pred. No. 1.6e+02;		
	Matches 40;	Conservative 0;	Mismatches 14;	Indels 0;	Gaps 0;
Oy	32	ATTAAATGCCCGCATATGTGAATGCTTAATACATTAATAAACGATATTC	85		
Dd	21	ATTACTTAGACCGCTTATGTGAATCACAGAAGACTCTCAAAGAAACAGATATTC	74		
RESULT 22	BG187125/c	802 bp	mRNA	linear	EST 21-Apr-2001
LOCUS	BG187125				

DEFINITION	RN6108 Athensys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION	BG187125
VERSION	BG187125.1 GI:33708812
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 802) Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothen,K., Lo,K., Offenbacher,J., Danzig,M., and Ducar,M. Creation of genome-wide protein expression libraries using random activation of gene expression Nat. Biotechnol. 19 (5), 440-445 (2001)
TITLE	JOURNAL MEDLINE PUBMED 21227151 11329013
COMMENT	Contact: Scott J. Cain Athensys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scaineathensys.com High quality sequence stop: 422. Location/Qualifiers 1..802 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /cell_line="HT1080" /clone_lib="Athensys RAGE Library" /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, In press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
FEATURES	BASE COUNT 222 a 172 c 166 g 242 t ORIGIN
source	
Query Match	30.5%; Score 31.4; DB 10; Length 802;
Best Local Similarity	64.4%; Pred. No. 1.7e+02;
Matches	Conservative 0; Mismatches 26; Indels 0; Gaps 0;
OY	13 ATAACTATTATATACAGCATTAATAGCCTCGCATATGTGAATTGCATATACAGTTAA 72   Db 463 ACAACCTTTTAAAGATATCATTTAACAGCACATCCCTTGCGAATTGGAAAAAGCGTTAAA 404
OY	73 AAAACGGTATTTTC 85   Db 403 AGAGACGCCCTTTC 391
RESULT 23	
BI475987	406 bp mRNA linear EST 27-AUG-2001
LOCUS	fp51a12.x3 zebrafish gridded kidney Danio rerio cDNA clone
DEFINITION	IMAGE:4759990 3', mRNA sequence.
ACCESSION	BI475987
VERSION	BI475987.1 GI:15308409
KEYWORDS	EST.
SOURCE	Danio rerio (zebrafish)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE	1 (bases 1 to 406) Clair,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schuck,R., Riltter,E.,
AUTHORS	

TITLE  
JOURNAL  
COMMENT  
Washu Zebrafish EST Project 1998  
Unpublished  
Contact: Stephen L. Johnson  
K., Stepcoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,  
Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,  
Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.  
and Wilson, R.



Matches	53:	Conservative	0:	Mismatches	37:	Indels	0:	Gaps	0:
QY	14	TAACAGTTTAATGACACCAATTAACTAGCTCTGCATATGTAATGCTTAATACAGTTAAAA	73						
Db	134	TAACATTTTAATGAGTCTTGCAAAAAAATTTCAAAATTCATCTAGATGATGAATTAAGT	75						
QY	74	AAAGCGATTTCCCTGCTTGACCAACA	103						
Db	74	AAGCAATTTTTCACCTCTCTCATAAACA	45						
RESULT 28									
CA036697/c									
LOCUS	CA036697	536 bp	mRNA	linear	EST 04-MAR-2003				
DEFINITION	salidb005008	reproductive Salmu salar	cDNA, mRNA sequence.						
ACCESSION	CA036697								
VERSION	CA036697.1	GI:24335681							
KEYWORDS	EST.								
SOURCE	Salmu salar	(Atlantic salmon)							
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Proteoanchopterygii; Salmoniformes; Salmonidae; Salmu.								
REFERENCE	1 (bases 1 to 536)								
AUTHORS	GRASP Consortium, Davidson, W.S., Koop, B.F. and http://web.uvic.ca/cbr/grasp.								
TITLE	A survey of Salmu salar transcripts from high complexity cDNA libraries								
JOURNAL	Unpublished								
COMMENT	Contact: Koop BF Centre for Biomedical Research University of Victoria PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada Tel: 250 472 4067 Fax: 250 472 4075 Email: bkoop@uvic.ca Centre for Biomedical Research, University of Victoria cDNA preparation and sequencing: Roberto Alberto, Marianne Beetz-Sargent, Maura Busby, Peter Hunt, Linda McInnell, BF Koop. bioinformatics: Gordon D Brown POLYA-yes.								
FEATURES									
source	Location/Qualifiers								
	1..536								
	/organism="Salmu salar"								
	/mol_type="mRNA"								
	/strain="McConnell"								
	/db_xref="taxon:8030"								
	/clone_id="reproductive"								
	/note="Vector: plbuescriptlisk+; Library Creator: Kristian R von Schalburg; Atlantic salmon tissue contributors: Carlo Biagi, Mitch Uh and Robert Devlin (DFO , Vancouver, B.C.), Simon Jones (PBS, Nanaimo, B.C.), Seespring Hatchery (Crofton, B.C.), Rachel Roper (University of Victoria)"								
BASE COUNT	173 a 116 c 84 g 163 t								
ORIGIN									
Query Match	29.9%	Score 30.8;	DB 14;	Length 536;					
Best Local Similarity	61.0%	Pred. NO. 2.4e+02;							
Matches	50:	Conservative	0:	Mismatches	32:	Indels	0:	Gaps	0:
QY	2	AAGTACGATGGAATGAGTTAATGACGAGCTTAAATGCGCTGCATATGTCGAATTCGTA	61						
Db	91	AAGTACGATGTAATGACGAGTACATGATGATGTTTGTATCTGCTGAATGTA	32						
QY	62	ATACAGTTAAAAAAGCGTATT	83						
Db	31	ATACATCAAAATACCAAGTTT	10						
RESULT 29									

[illegible]





DEFINITION	CH230-271012.TVB CHORI-230 Segment 2 Rattus norvegicus genomic clone CH230-271012, genomic survey sequence.
ACCESSION	B2220889
VERSION	B2220889.1 GI:23879247
KEYWORDS	GSS.
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE	1 (bases 1 to 704) Zhao S., Shetty J., Shatsman S., Tseng G., Geer K., Shvartsbeyn A., Gebregeorgis E., Overton L., Russell D., Chen D., Riggs F., de Jong P. and Fraser C.M. Rat BAC End Sequences from Library CHORI-230 MboI segment Unpublished Other GSSs: CH230-271012.TVB
TITLE	Contact: Shaying Zhao
JOURNAL	Department of Eukaryotic Genomics
COMMENT	The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel.: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the rat BAC library CHORI-230 ( <a href="http://www.chori.org/bacpac/rat230.htm">http://www.chori.org/bacpac/rat230.htm</a> ). For BAC library availability, please contact Pieter de Jong ( <a href="mailto:pdejong@mail.cho.org">pdejong@mail.cho.org</a> ). Clones may be purchased from BACPAC Resources ( <a href="http://www.chori.org/bacpac/orering_information.htm">http://www.chori.org/bacpac/orering_information.htm</a> ). BAC end page: <a href="http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html">http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html</a> Plate: 271 row: 0 column: 12 Seq primer: SP6 Class: BAC ends.
FEATURES	Location/Qualifiers
SOURCE	1..704 /organism="Rattus norvegicus" /mol_type="genomic DNA" /strain="BN/SSNhd/MCM" /db_xref="taxon:10116" /clone="CH230-271012" /sex="Female" /cell_type="Brain" /clone_id="CHORI-230 Segment 2" /note="Vector: pPARBAC1.3; Site_1: MboI; site_2: MboI; CHORI-230 Rat (BN/SSNhd/MCM) BAC library produced by Pieter de Jong"
BASE COUNT	203 a         118 c         131 g         252 t
ORIGIN	
Query Match	29.7%; Score 30.6; DB 29; Length 704;
Best Local Similarity	58.1%; Pred. No. 2, Be+02;
Matches	54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
Db	11 GAATACAGTTTAATGACAGCATTAATGCTCGATATGTGAATTGTAATACAGTAA 70   52 GAAAAAACAATGATAAGAAGACAGATTAATAAACAAATCATGTGGATAATAGATTATGAC 111  71 AAAAAACGGTATTTCCTCGTGTCGATCCACA 103   112 CAATTCATTGTTTCTCGTATCCTTTCAAAA 144
RESULT 35	
LOCUS	BUB853968 785 bp mRNA linear EST 16-Oct-2002
DEFINITION	AGNCOCURF_10403096 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6621037
ACCESSION	BUB853968
VERSION	BUB853968.1 GI:24038934
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



```

/mol_type="mRNA"
/db_xref="taxon:39946"
/clone="BR060006B20E09.ab1"
/tissue_type="Panicles"
/dev_stage="Flowering"
/clone_lib="IRRI clones"
/notes="Vector: pBluescript II SK+; Water stress was
applied by not watering for 4 consecutive days. Panicles
were collected from control (well watered) and stressed
plants at 2 days before heading, heading, 50% flowering
and 4 days after 50% flowering."

BASE COUNT      205 a      151 c      132 g      214 t
ORIGIN

Query Match      29.5%; Score 30.4; DB 14; Length 702;
Best Local Similarity 67.2%; Pred. No. 3.2e+02;
Matches 43; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY      13 ATACAGTTTATGACGATTATAGCTCTGCATATGTAATGCTAATACAGTTAA 72
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      73 ATACAGATTACTAGTAATACATATATATCTGCATGATATTGAGATCAAAAAA 14
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      73 AAAA 76
        ||||
DB      13 AAAA 10

RESULT 38
CNS02AXT/LOCUS      908 bp      DNA      linear      GSS 01-SEP-2000
DEFINITION      Tetradon nigriviridis genome survey sequence PUC-Or1 end of clone
                252F17 of library G from Tetradon nigriviridis, genomic survey
                sequence.
ACCESSION      AL189146
VERSION      AL189146.1 GI:7827250
KEYWORDS      GSS: genome survey sequence.
SOURCE      Tetradon nigriviridis
ORGANISM      Tetradon nigriviridis
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                Tetraodontidae; Tetraodontidae; Tetraodon.
REFERENCE      1 Roest Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,
                Bernot, A., Fitzames, C., Wincker, P., Brothier, P., Quetier, F.,
                Sautin, W. and Weissenbach, J.
                Estimate of human gene number provided by genome-wide analysis
                using Tetradon nigriviridis DNA sequence
                Nat. Genet. 25 (2), 235-238 (2000)
JOURNAL
MEDLINE      20296633
PUBMED      10835645
REFERENCE
AUTHORS      Roest Crolius, H., Jallion, O., Dasilva, C., Ozouf-Costaz, C.,
                Fitzames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,
                Sautin, W., Bernot, A. and Weissenbach, J.
                Characterization and repeat analysis of the compact genome of the
                freshwater pufferfish Tetradon nigriviridis
                Genome Res. 10 (7), 939-949 (2000)
JOURNAL
MEDLINE      20359837
PUBMED      10899143
REFERENCE
AUTHORS      Genoscope.
                3 (bases 1 to 908)
                Direct Submision
                Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
                BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                - Web : www.genoscope.cns.fr)
                This sequence is a single read and was generated as part of a large
                scale clone-end sequencing project of the Tetradon nigriviridis
                genome. For more information, please take a look at
                http://www.genoscope.cns.fr/Tetradon.
                Location/Qualifiers
                source
                1..908

```

```

/organism="Tetradon nigriviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="252F17"
/clone_lib="G"
/notes="Genoscope sequence ID : C0AG252CC09SP1-end :
PUC-Or1"

BASE COUNT      286 a      176 c      212 g      233 t      1 others
ORIGIN

Query Match      29.5%; Score 30.4; DB 29; Length 908;
Best Local Similarity 59.8%; Pred. No. 3.4e+02;
Matches 49; Conservative 1; Mismatches 32; Indels 0; Gaps 0;

QY      6 GACTGGAATACAGTTTATGACAGCAATATAGCTCTGCATATGTAATGCTAATAC 65
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      907 GACTGCAATMAAATTTATCTAATATATATTTAGCGCTTGTAATATATCTAATTC 848
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      66 AGTTAAAAAAGCGTATTTCCC 87
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      847 ATCTCAATATACCGTATTTGCC 826
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 39
AM250036/C LOCUS      479 bp      mRNA      linear      EST 07-JAN-2000
DEFINITION      2819291.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819291 3',
                mRNA sequence.
ACCESSION      AM250036
VERSION      AM250036.1 GI:6593029
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      1 (bases 1 to 479)
                NIH-MGC http://mgc.nci.nih.gov/
                National Institutes of Health, Mammalian Gene Collection (MGC)
                Unpublished
                Other ESTs: 2819291.5prime
                Contact: Robert Strausberg, Ph.D.
                Email: cgabs-remail.nih.gov
                Tissue Procurement: DCTD/DRP cDNA library preparation: Ling
                Hong/Rubin laboratory cDNA library Arrayed by: The I.M.A.G.E.
                Consortium (LMNL) DNA Sequencing by: Berkeley MGC sequencing
                project Clone distribution: MGC clone distribution information can
                be found through the I.M.A.G.E. Consortium/LMNL at:
                www.bio.llni.gov/brp/image/image.html Base calling / Quality
                Scores: PHRED from University of Washington Genome Center. Vector
                trimming: cross-match from University of Washington Genome Center
                PHRAP suite. Poly-T identification: patmatch.pl from Berkeley
                Drosophila Genome Project. University of Washington Genome Center:
                http://www.genome.washington.edu/polyadenylation: Based upon the
                presence of a XhoI site followed by a run of 14 or more T residues
                at the beginning of the sequence, this cDNA insert was
                polyadenylated.
                Plate: LCCM row: D column: 12
                High quality sequence stop: 376.
                Location/Qualifiers
                1..479
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:2819291"
                /tissue_type="small cell carcinoma"
                /cell_line="MGC3"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_7"
                /note="Organ: lung; Vector: pORF7; Site_1: XhoI; Site_2:
                EcoRI; cDNA made by oligo-dT priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGCACGAG(G). Size-selected >500bp for genome
                insert size 1.8kb. Library constructed by Ling Hong in

```

Oy 23 AATGACAGCATTAACTAGCTCCGCATATGTGAATTGTAATACAGTTAAAAAACCGGTAT 82  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 41 AAGAACACTCACTAAAAGCTCAAGCATTAAGTAGACCAACAATAATGTGAAAAAAAAACCCCTAT 100

QY 83 TTCCCTGTTTCATGCCA 100  
 Db 101 GTCCACACAGCTCTGGCAA 118

RESULT 42  
 BH002214/c 382 bp DNA linear GSS 04-MAY-2001  
 LOCUS BH002214/c  
 DEFINITION BMBAC02B16SP6.PSU Brugia malayi Genomic Bac Library 1 & 2 Brugia  
 ACCESSION BH002214  
 VERSION BH002214.1 GI:13941603  
 KEYWORDS GSS.  
 SOURCE Brugia malayi  
 ORGANISM Brugia malayi  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
 Onchocercidae; Brugia.  
 1 (bases 1 to 382)  
 Whitton,C., Daub,J., Ware,J., Quail,M., Hall,N., Barrell,B., Foster  
 J., Guillano,D., Slatko,B. and Blaxter,M.  
 Genome survey sequences from the human parasitic nematode Brugia  
 malayi  
 JOURNAL Unpublished  
 COMMENT Contact: Blaxter ML  
 Institute of Cell, Animal and Population Biology  
 University of Edinburgh  
 Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9  
 3JT, UK  
 Tel: +44 131 650 6760  
 Fax: +44 131 670 5450  
 Email: mark.blaxter@ed.ac.uk

FEATURES  
 source  
 Location/Qualifiers  
 1..382  
 /organism="Brugia malayi"  
 /mol\_type="genomic DNA"  
 /strain="TRS"  
 /db\_xref="taxon:6279"  
 /sex="Mixed (male and female)"  
 /tissue\_type="whole parasite"  
 /dev\_stage="adult"  
 /clone\_lib="Brugia malayi Genomic Bac Library 1 & 2"  
 /note="Vector: pBelobAC II; Site\_1: Hind III; Brugia  
 malayi genomic DNA was partially cleaved with Hind III and  
 size fractionated. 18,000 clones were generated from 2  
 libraries with mean insert size 60 kbp. The library was  
 constructed by Jesse Pope-Chappel, Smith College  
 Northampton MA and Dr Jeremy Foster, New England Biolabs,  
 MA."

BASE COUNT 134 a 73 c 43 g 131 t 1 others

ORIGIN  
 Query Match 29.1%; Score 30; DB 28; Length 382;  
 Best Local Similarity 64.3%; Pred. No. 3.7e+02;  
 Matches 45; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 7 ACTGGAATAACGTTTAATGACAGCATTAATAGCTCCGATATGTAATGCTAATACA 66  
 Db 308 ACTGATAGATAAATTAATGAGAAATTATACGCTAGCTAGTATGTAATATACA 249

QY 67 GTTAAAAA 76  
 Db 248 GTTAAAAA 239

RESULT 43

AZ460533/c 592 bp DNA linear GSS 04-OCT-2000  
 LOCUS AZ460533  
 DEFINITION 1M0265H22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0265H22 R, genomic survey sequence.  
 ACCESSION AZ460533  
 VERSION AZ460533.1 GI:10618658  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 Mammalia; Euthera; Rodentia; Scurionath; Muridae; Murinae; Mus.  
 1 (bases 1 to 592)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly  
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
 and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0265 row: H column: 22  
 Seq primer: CACACAGCAAAACAGCTATGACCC  
 Class: plasmid ends  
 High quality sequence stop: 592.

FEATURES  
 source  
 Location/Qualifiers  
 1..592  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0265H22"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv: Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMDA2 (gii473211419b1aF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 179 a 145 c 111 g 156 t 1 others

ORIGIN  
 Query Match 29.1%; Score 30; DB 28; Length 592;  
 Best Local Similarity 67.7%; Pred. No. 4e+02;  
 Matches 42; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 28 CAGCATTAATAGCTCTGCATATGTAATGCTAATACGTTAAAAACGGATTTCCTCC 87  
 Db 133 CAGCATTAATAGATATACATGATTAATTAATTCCTCCATTCACATCAACAAAGCATTTGCG 74

QY 88 TG 89

Db 73 TG 72

RESULT 44  
BH294981/c  
LOCUS  
DEFINITION BH294981 612 bp DNA linear GSS 30-NOV-2001  
CH230-186011.T3 CHORI-230 Segment 1 Rattus norvegicus genomic clone  
CH230-186011, genomic survey sequence.  
BH294981  
VERSION BH294981.1 GI:17207389  
KEYWORDS GSS.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 612)  
Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn  
A., Gebregorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de  
Jong, P. and Fraser, C. M.  
Rat BAC End Sequences from Library CHORI-230 EcORI segment  
Unpublished  
COMMENT Other\_GSSs: CH230-186011.TV  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the rat BAC library CHORI-230  
(http://www.chori.org/bacpac/rat230.htm). For BAC library  
availability, please contact Pieter de Jong (pdejong@email.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/or ordering information.htm). BAC end  
plate: http://www.tigr.org/tldb/Bac\_ends/rat/Bac\_end\_intro.html  
Plate: 186 row: 0 column: 11  
Seq primer: SP6  
Class: BAC ends.  
Location/Qualifiers  
1. 612  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/strain="BN/SSNHsd/MCg"  
/db\_xref="taxon:10116"  
/clone="CH230-186011"  
/sex="Female"  
/cell\_type="Brain"  
/clone\_lib="CHORI-230 Segment 1"  
/note="Vector: pTARBAC2.1; Site\_1: EcORI; Site\_2: EcORI;  
CHORI-230 Rat (BN/SSNHsd/MCg) BAC library produced by  
Pieter de Jong"

BASE COUNT 193 a 115 c 103 g 201 t

ORIGIN

Query Match 29.1%; Score 30; DB 28; Length 612;  
Best Local Similarity 59.3%; Pred. No. 4.1e+02;  
Matches 51; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 12 AATAACGTTTAATGACAGCATTAATGCTCGATGATGTAATGCAATACAGTTAA 71  
|||||  
DB 407 AATCAGATTAATATATGTTACAAACATCATGTGATGATGTTTAAAGATTA 348  
|||||  
QY 72 AAAAAGCGTATTTCCCTGCTCTGAT 97  
|||||  
DB 347 AGAAGGATATGTCCAGGGTTTGGT 322  
|||||

RESULT 45  
A2496877/c  
LOCUS A2496877 688 bp DNA linear GSS 05-OCT-2000  
DEFINITION 1M0333D03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION A2496877  
VERSION A2496877.1 GI:10673385  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 688)  
Dunn, D., Aoyagi, A., Barber, M., Beacroft, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Petersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10Kb  
plasmid inserts  
Unpublished  
CONTACT: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0333 row: D column: 03  
Seq primer: CACACAGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 688.  
Location/Qualifiers  
1. 688  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0333D03"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, p1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g11473211419b1AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 191 a 142 c 123 g 231 t

ORIGIN

Query Match 29.1%; Score 30; DB 28; Length 688;  
Best Local Similarity 57.4%; Pred. No. 4.2e+02;  
Matches 54; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 5 TGACGTGAATACAGTTTAATGACAGCATTAATGCTCGATGATGTAATGCTAATA 64  
|||||  
DB 437 TAACAGGATTTTATGTTTCTAACCTCATGTAATGATGTAATGATGTAATGCTCCTAGCA 378  
|||||  
QY 65 CAGTTAAAAAAGCGTATTTCCCTGCTCTGATC 98  
|||||  
DB 377 CAGAAAAAATATCTACTGCTCTGATGCTCTTC 344  
|||||

Wed Aug 27 07:55:37 2003

us-09-693-205a-7\_6543\_6645.aug20.rst

Page 21

Search completed: August 25, 2003, 07:49:37  
Job time : 1653 secs

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